

GenCore version 5.1.4 p5 4578  
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CM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 17:37:19 ; Search time 177 Seconds  
(without alignments)  
10560.218 Million cell updates/sec

File: US-09-358-321c-31

Perfect score: 830

Sequence: 1 tctagaatggttaagcgctat.....ctgaattagtagcgccgcg 830

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_101002:\*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
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- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
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- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	830	100.0	830	21	AAZ61047
2	528	63.6	828	21	AAA92439
3	528	63.6	828	22	AAH78144
4	528	63.6	828	24	ABK71323
5	528	63.6	828	24	ABA04520
6	526.4	63.4	828	21	AAA92443
7	526.4	63.4	828	22	AAH78148
8	526.4	63.4	828	24	ABK71327
9	526.4	63.4	828	24	ABA04524

10	521.4	62.8	819	21	AAA92442	Plasmid pCHOM1 MAB
11	521.4	62.8	819	22	AAH78147	Nucleotide sequenc
12	521.4	62.8	819	24	ABK71326	DNA encoding throm
13	521.4	62.8	819	24	ABA04523	Murine MABL-1 #4 c
14	519.8	62.6	819	21	AAA92444	Plasmid pCHOM2 MAB
15	519.8	62.6	819	22	AAH78149	Nucleotide sequenc
16	519.8	62.6	819	24	ABK71328	DNA encoding throm
17	519.8	62.6	819	24	ABA04525	Murine MABL-2 #4 c
18	518.4	62.5	1605	22	AAH78156	Nucleotide sequenc
19	518.4	62.5	1605	24	ABK71335	DNA encoding throm
20	518.4	62.5	1605	24	ABA04532	Murine MABL-2 #6 c
21	512.4	61.7	741	22	AAH78153	Nucleotide sequenc
22	512.4	61.7	741	22	ABK71332	DNA encoding throm
23	512.4	61.7	741	24	ABA04529	Murine MABL-2 #5 c
24	510.8	61.5	876	19	AAV10390	Monoclonal antibod
25	501.2	60.4	1637	21	AAZ88358	Bispecific anti-ze
26	499	60.1	753	20	AAZ77245	Mouse scFV fragmen
27	499	60.1	753	20	AAZ77241	Mouse scFV fragmen
28	486	58.6	780	22	AAH78172	Nucleotide sequenc
29	486	58.6	780	24	ABK71351	DNA encoding throm
30	486	58.6	780	24	ABA04548	Murine MABL-2 #7 c
31	476	57.3	753	22	AAF60025	DNA encoding singl
32	476	57.3	792	22	AAF60021	DNA encoding S19 S
33	447	53.9	459	21	AAZ61045	Nucleotide sequenc
34	444	53.5	792	22	AAF60022	DNA encoding singl
35	443.4	53.4	786	22	AAF60026	DNA encoding singl
36	423.4	51.0	438	21	AAZ61046	Nucleotide sequenc
37	419.4	50.5	1135	20	AAZ58936	Plasmid pJG718 enc
38	415	50.0	1047	20	AAZ21156	Artificial synthe
39	415	50.0	1086	20	AAZ21158	Artificial synthe
40	411.6	49.6	768	17	AAZ48000	Coding sequence fo
41	409.4	49.3	729	19	AAZ36236	DNA of ScFv 421 wh
42	408.2	49.2	753	21	AAZ61064	Heavy chain of an
43	407.6	49.1	749	18	AAZ6234	Anti-human protein
44	405.2	48.8	1611	18	AAZ86221	Human p53 protein
45	401.4	48.4	726	20	AAZ86942	Antibody B10C7 enc

#### ALIGNMENTS

RESULT 1  
AAZ61047  
ID AAZ61047 standard; DNA; 830 BP.  
XX  
AC AAZ61047;  
XX  
DT 30-MAY-2000 (first entry)  
XX  
DE DNA encoding a single chain anti-delta9-desaturase antibody.  
XX  
KW Delta9-desaturase; antibody; transit peptide; passenger protein;  
KW plant cell organelle; maize; stearoyl-ACP-delta9-desaturase;  
KW transgenic plant; ss.  
XX  
OS Synthetic.  
OS Mus sp..  
XX  
FH Key  
FH CDS  
FT Location/Qualifiers  
FT 7..813  
FT /tag= a  
FT /note= "no termination codon given"  
FT 67..813  
FT /tag= b  
XX  
PN WO200005391-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 21-JUL-1999; 99WO-US16405.  
XX  
PR 21-JUL-1998; 98US-0093587.  
XX

(DOWC ) DOW AGROSCIENCES LLC.  
Sukhapinda K, Hasler JM, Petell JK, Strickland JA, Folkerts O;  
WPI: 2000-182711/16.  
P-PSDB; AAY68992.  
Novel nucleic acid construct for down-regulating steady state levels of proteins in plant cells, transgenic plants and their progeny -  
Claim 21; Page 95-96; 114pp; English.  
The present sequence encodes a single chain antibody which is directed against a Zea mays (maize) delta9-desaturase. The sequence is used to produce the constructs of the invention. These constructs encode an antibody that can bind a transit peptide that directs an associated passenger protein to a plant cell organelle. The transit peptide sequence of the maize stearyl-ACP-delta9-desaturase (delta9-desaturase) was determined, and used to produce antibodies of the invention. These antibodies were produced in transgenic plants of the invention. The constructs of the invention are useful for producing antibodies which decrease steady state levels of passenger proteins in the organelles of plant cells and plants, by binding to the transit peptide. This results in the production of transgenic plants which have altered steady state passenger protein levels.  
Sequence 830 BP; 207 A; 200 C; 221 G; 202 T; 0 other;  
Query Match 100.0%; Score 830; DB 21; Length 830;  
Best Local Similarity 100.0%; Pred. No. 3.9e-225;  
Matches 830; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 TCTAGATGGTAAAGCGCTATTGTTTATATGCTTTTGGCGCGCGCGCATTTCTGCC 60  
1 TCTAGATGGTAAAGCGCTATTGTTTATATGCTTTTGGCGCGCGCGCATTTCTGCC 60  
61 TTTGGCGGGTTCACATGCAGCAGTCTGGGGCTGAGCTGGTGAAGCTTCACTG 120  
61 TTTGGCGGGTTCACATGCAGCAGTCTGGGGCTGAGCTGGTGAAGCTTCACTG 120  
121 AGCTGTCTCGAAGCTTCGGGCTACACATTTACTGACTATGAATACATGGGTGAGG 180  
121 AGCTGTCTCGAAGCTTCGGGCTACACATTTACTGACTATGAATACATGGGTGAGG 180  
181 CAGACACCTGTGCATGGCTCGAATGGATTGGAGCTATTGATCTGAAACTGGTGGTACT 240  
181 CAGACACCTGTGCATGGCTCGAATGGATTGGAGCTATTGATCTGAAACTGGTGGTACT 240  
241 GCCTCAATCAGAACTTCAAGGACAAGGCCATAGTGAAGTATGCTTCCAGCACA 300  
241 GCCTCAATCAGAACTTCAAGGACAAGGCCATAGTGAAGTATGCTTCCAGCACA 300  
301 GCCTACATGGAGCTCCGAGCTGACATCTGAAGCTCTGGCTCTATTACTATACAGA 360  
301 GCCTACATGGAGCTCCGAGCTGACATCTGAAGCTCTGGCTCTATTACTATACAGA 360  
361 TGGTTTGGAGCTGGGGCCAAAGGACTCTGGTCACTGCTCTGCAGAGGTAATCTCTCA 420  
361 TGGTTTGGAGCTGGGGCCAAAGGACTCTGGTCACTGCTCTGCAGAGGTAATCTCTCA 420  
421 GGATCTGGCTCCGAATCCAAACCCCGGGATGTTGTGATGAGCCCCAAACCCCTCTCC 480  
421 GGATCTGGCTCCGAATCCAAACCCCGGGATGTTGTGATGAGCCCCAAACCCCTCTCC 480  
481 CCTGTCACTCTGGAGATCAGCTCCATCTCTTGCAGATCTAGTCAGAGCTTTTACAC 540  
481 CCTGTCACTCTGGAGATCAGCTCCATCTCTTGCAGATCTAGTCAGAGCTTTTACAC 540  
541 AGTAATGGAATCACCTATTATGATGGTACCTGCGAAGCCAGGCGCAGTCTCCAAAGCTC 600  
541 AGTAATGGAATCACCTATTATGATGGTACCTGCGAAGCCAGGCGCAGTCTCCAAAGCTC 600  
601 CTGATCTCAAAAGTTTCCAAACCGATTTTCTGGGGTCCCGACAGAGGTTCAAGTGGCAGTGG 660

Db 601 CTGATCTCAAAAGTTTCCAAACCGATTTTCTGGGGTCCCGACAGAGTTCAGTGGCAGTGG 660  
Qy 661 TCAGGACAGATTTTCACTCAAGATCAGCAGAGTGGAGCTGAGGATCTGGGAGTTTAT 720  
Db 661 TCAGGACAGATTTTCACTCAAGATCAGCAGAGTGGAGCTGAGGATCTGGGAGTTTAT 720  
Qy 721 TTTCTCTCTCAAAAGTACACATGTTCCGTACACAGTTCGAGGGGGGACCAAGCTGGAATA 780  
Db 721 TTTCTCTCTCAAAAGTACACATGTTCCGTACACAGTTCGAGGGGGGACCAAGCTGGAATA 780  
Qy 781 AAAGAGAAAAAATCTATCTCAGAGAGGATCTGAATAGTAAGCGGCGC 830  
Db 781 AAAGAGAAAAAATCTATCTCAGAGAGGATCTGAATAGTAAGCGGCGC 830  
RESULT 2  
AAA92439  
ID AAA92439 standard; DNA; 828 BP.  
XX  
AC AAA92439;  
XX  
DT 15-JAN-2001 (first entry)  
XX  
DE Plasmid pscM1 MABLI-scfv nucleotide sequence SEQ ID NO:20.  
XX  
KW Monoclonal antibody; MABL; IAP; integrin associated protein;  
KW Single stranded Fv; apoptosis; blood disease; leukaemia;  
KW Cytostatic; ds.  
XX  
OS Mus sp.  
XX  
PN WO200053634-A1.  
XX  
PD 14-SEP-2000.  
XX  
PF 10-MAR-2000; 2000WO-JP01458.  
XX  
PR 10-MAR-1999; 99JP-0063557.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Fukushima N, Uno S;  
XX  
WPI: 2000-587428/55.  
P-PSDB; AAB23817.  
XX  
Single stranded Fv antibody fragment inducing apoptosis in nucleated blood cells having integrin associated protein for treatment of leukemia -  
Example 5; Page 59-61; 73pp; Japanese.  
XX  
The present invention describes a polypeptide containing the variable region of the light chain of a monoclonal antibody, which induces apoptosis in nucleated blood cells having integrin associated protein (IAP). Also described are: (1) DNA encoding the novel polypeptide; (2) animal or microbial cells expressing the DNA of (1); and (3) agents for the treatment of blood disorders which contain the polypeptide. The polypeptide can be used in the treatment of blood disorders such as leukaemia. The present sequence encodes the protein sequence from pscM1 MABLI-scfv, which is used in an example from the present invention.  
XX  
SQ Sequence 828 BP; 211 A; 201 C; 223 G; 193 T; 0 other;  
Query Match 63.6%; Score 528; DB 21; Length 828;  
Best Local Similarity 82.9%; Pred. No. 1.5e-139;  
Matches 632; Conservative 0; Mismatches 115; Indels 15; Gaps 2;  
Qy 46 GCGGCGCATTTCTGCGCTTTGGCGGGTTCAACATCGAGCAGTCTGGGCTGAGCTGGTGG 105  
Db 46 GCTGCCCAACCGCCATGGCGCAGGTCCAGCTGACAGCAGTCTGACCTGACCTGGTAAAG 105



511 TCTTGACAGTCTAGTCAGAGCCTTTTACACAGTAATGAATCACCTATTATACATTGGTAC 570  
 526 TCTTGACAGTCTAGTCAGAGCCTTTTACACAGTAATGAATCACCTATTATACATTGGTAC 585  
 571 CTGACAGAGCCAGGCGAGTCTCAAGAGCTCTGATCTACAAAGTTTCCAAACCGATTTCCT 630  
 586 CTACAGAGCCAGGCGAGTCTCAAGAGCTCTGATCTACAAAGTTTCCAAACCGATTTCCT 645  
 631 GGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACACTCAGATCAGC 690  
 646 GGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACACTCAGATCAGC 705  
 691 AGAGTGGAGGCTGAGGATCTGGAGGTTTATTTCTGCTCTCAAAAGTACACATGTTCCGGTAC 750  
 706 AGAGTGGAGGCTGAGGATCTGGAGGTTTATTTCTGCTCTCAAAAGTACACATGTTCCGGTAC 765  
 751 ACCTTGGAGGGGGGACCAAGCTGGAAATAAAGAGAAAAA 792  
 766 ACCTTGGAGGGGGGACCAAGCTGGAAATAAAGAGACTACAAA 807

## RESULT 4

ABK71323  
 ID ABK71323 standard; DNA; 828 BP.

ABK71323;

30-JUL-2002 (first entry)

DNA encoding thrombopoietin agonist antibody associated protein #5.

Modified antibody; thrombopoietin; TPO; agonist;

TPO receptor; platelet reduction-associated blood disease;

thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction; gene; ds.

Mus sp.

WO200233072-A1.

25-APR-2002.

22-OCT-2001; 2001WO-JP09259.

20-OCT-2000; 2000JP-0321821.

17-APR-2001; 2001WO-JP03288.

12-SEP-2001; 2001JP-0277314.

(CHUS) CHUGAI SEIYAKU KK.

Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;

WPI: 2002-383513/41.

P-PSDB; ABG35311.

Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia

Example 5; Page 147-148; 213pp; Japanese.

The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This sequence encodes a thrombopoietin (TPO) agonist antibody associated protein.

SQ Sequence 828 BP; 211 A; 201 C; 223 G; 193 T; 0 other;  
 Query Match 63.6%; Score 528; DB 24; Length 828;  
 Best Local Similarity 82.9%; Pred. No. 1.5e-139;  
 Matches 632; Conservative 0; Mismatches 115; Indels 15; Gaps 2;

QY 46 GCGGCGCATCTGCGCTTTGGCGGCTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGAGG 105  
 DB 46 GCTGCCAACACAGCCATGGCGCAGGTCAGCTGCAGCAGCTGCGACCTGACCTGGTAAAG 105  
 QY 106 CTTGGGGCTTCACTGACGCTGCTCTGCAAGGCTTTCGGGCTACACATTTTACTGACTATGAA 165  
 DB 106 CTTGGGGCTTCACTGACGCTGCTCTGCAAGGCTTTCGGGCTACACATTTTACTGACTATG 165  
 QY 166 ATACACTGGGTGAGCAGACACCTGTGCATGGCCCTGGATGGATGGAGCTATTGATCT 225  
 DB 166 ATGCACTGGGTGAGCAGACAGCCAGGCGAGGCTTGGATGGATGATATATTTATCT 225  
 QY 226 GAAACTGGTGGTACTGCTTACAAATCAGAAAGTTTCAAGGCAAGGCCATAGTGACTGTAGAC 285  
 DB 226 TACAATGATGGTACTAAGTACAAATCAGAAAGTTTCAAGGCAAGGCCATAGTGACTGTAGAC 285  
 QY 286 AAATCCTCAGCAGCCTTACATGGAGCTTCGCGCCTGACATCTTGAAGACTCTCCGCTC 345  
 DB 286 AAATCCTCAGCAGCCTTACATGGAGCTTCGCGCCTGACATCTTGAAGACTCTCCGCTC 345  
 QY 346 TATTACTATACAGATGG-----TTTGGAGCTGGGGCAAGGGACTCTGGTC 393  
 DB 346 TACTACTGTGCAAGAGGGGGTTACTATAGTTACGACGACTGGGGCAAGGGCACTCTC 405  
 QY 394 ACTGTCTCTGCA---GAGGTAAATCCTCAGGATCTGGCTCCGAATCCAAACCCGGGAT 450  
 DB 406 ACAGTCTCTCAGTGGTGGTGGTTCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 465  
 QY 451 GTTGTGATGACCCCAACCCACTCTCCCTGCTGTGAGTCTTTGGAGATCAAGCCTCCATC 510  
 DB 466 GTTGTGATGACCCCAACCCACTCTCCCTGCTGTGAGTCTTTGGAGATCAAGCCTCCATC 525  
 QY 511 TCTTCAGATCTAGTCAGAGCCTTTTACACAGTATGAATCACTATTACATTTGGTAC 570  
 DB 526 TCTTCAGATCTAGTCAGAGCCTTTTACACAGTATGAATCACTATTACATTTGGTAC 585  
 QY 571 CTGACAGAGCCAGGCGAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTCCT 630  
 DB 586 CTACAGAGAGCCAGGCGAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTCCT 645  
 QY 631 GGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACACTCAAGATCAGC 690  
 DB 646 GGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACACTCAAGATCAGC 705  
 QY 691 AGAGTGGAGGCTGAGGATCTGGAGTGTATTTCTGCTCTCAAGGTACACATGTTCCGGTAC 750  
 DB 706 AGAGTGGAGGCTGAGGATCTGGAGTGTATTTCTGCTCTCAAGGTACACATGTTCCGGTAC 765  
 QY 751 ACGTTCCGAGGGGGGACCAAGCTGGAAATAAAGAGAAAAA 792  
 DB 766 ACGTTCCGAGGGGGGACCAAGCTGGAAATAAAGAGACTACAAA 807

## RESULT 5

ABA04520

ID ABA04520 standard; DNA; 828 BP.

XX ABA04520;

XX ABA04520;

DT 15-FEB-2002 (first entry)

DE Murine MABL-1 #3 coding sequence.

XX Murine; cytostatic; antiinflammatory; antianaemic; vasotropic;

XX antibody; signal transduction; cancer; inflammation; hormonal disorder;

XX leukaemia; lymphoma; aplastic anaemia; skeletal malformation; ds.

XX



OS Mus sp.  
 XX Key Location/Qualifiers  
 FH CDS 1..825  
 FT /\*tag= a  
 FT /product= "MURINE MABU-1 #3"  
 XX  
 PN W0200179494-A1.  
 XX 25-OCT-2001.  
 XX 17-APR-2001; 2001WO-JP03288.  
 XX 17-APR-2000; 2000JP-0115246.  
 PR 20-OCT-2000; 2000JP-0321821.  
 PR 20-OCT-2000; 2000JP-0321822.  
 PR 12-MAR-2001; 2001WO-JP01912.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;  
 PI P-PSDB; AAM47631.  
 XX WPI; 2002-066368/09.  
 DR Antibodies for treatment of diseases associated with cell  
 PT proliferation, hormonal disorders and cytokines comprise agonist  
 PT activity to signal transmission across cell membranes -  
 XX  
 XX Example 5; Page 126-128; 173pp; Japanese.  
 XX The present invention relates to modified antibodies. The antibodies  
 CC contain two or more H chain V domains and two or more L chain V domains  
 CC of a monoclonal antibody (MAB) which is capable of transmitting a signal  
 CC across the cell membrane by cross-linking a cell surface molecule, where  
 CC the antibodies can serve as signal transmission agonists. The antibodies  
 CC are useful for treatment and prevention of a broad range of disorders in  
 CC which signal transmission is implicated, such as cancer, inflammation,  
 CC hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and  
 CC skeletal malformations. The present sequence was used to illustrate the  
 CC present invention.  
 XX  
 SQ Sequence 828 BP; 211 A; 201 C; 223 G; 193 T; 0 other;

Query Match 63.6%; Score 528; DB 24; Length 828;  
 Best Local Similarity 82.9%; Pred. No. 1.5e-139;  
 Matches 632; Conservative 0; Mismatches 115; Indels 15; Gaps 2;

QY 46 GCGGCGATTCTGCTTTGGCGGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTCAGG 105  
 DB 46 GCTGCCCAACGAGCCATGGCGCAGGTCCAGCTGCAGCAGTCTGGACCTGGTAAAG 105  
 QY 106 CTTGGGGCTTCAGTGACGCTCTCTGCAAGGCTTCGGGCTACACATTTACTGACTATGAA 165  
 DB 106 CTTGGGGCTTCAGTGAAAGTCTCTGCAAGGCTTCGGGCTACACATTTCTGTAACCATGTT 165  
 QY 166 ATACACTGGGTGAGGCGACACACCTGTGCATGGCTGGAATGGAATGGAGCTATTGATCCT 225  
 DB 166 ATGCACTGGGTGAGGCGACAGCCAGGCGAGGCTTCAGTGGATTGATATATTTATCCT 225  
 QY 226 GAACTGGTGTACTGCTACATCAATCAGAACTTCAAGGCAAGGCGCATAGTACTGTAGAC 285  
 DB 226 TACAATGATGGTACTAAGTACAATGAGAAGTTCAGGCGCAAGGCGCACACTGCTTCAGAG 285  
 QY 286 AATCTCTCCAGCAGCCTACATGAGCTCCGAGCTCGACATCTGAAGACTCTGCGGTC 345  
 DB 286 AATCTCTCCAGCAGCCTACATGAGCTCGACATCTGAGGCTCTGAGGCTCTGCGGTC 345  
 QY 346 TATTACTATCAAGATGG-----TTTGAGGACTGGGSCCAAGGACTCTGGTC 393  
 DB 346 TACTACTGTGCAAGAGGGGGTTACTATAGTTACGACACTGGGSCCAAGGCAACCACTCTC 405  
 QY 394 ACTGCTCTGCA----GAGGGTAAATCTCTAGGATCTGGCTCCCGAATCCAAACCGGGGAT 450

DB 406 ACAGTCTCTCAGTGGTGGTTCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 465  
 QY 451 GTTGTGATGACCCCAAAACCCACTCTCCCTGCCTGTGTCAGTCTTGGAGATCAAGCTCCATC 510  
 DB 466 GTTGTGATGACCCCAAAACTCCACTCTCCCTGCCTGTGTCAGTCTTGGAGATCAAGCTCCATC 525  
 QY 511 TCTTGAGATCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCT 570  
 DB 526 TCTTGAGATCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCT 585  
 QY 571 CTGCAAGACCCAGGCGGCTCTCCAAAGCTCTCCAAAGCTCTCCAAAGCTCTCCAAAGCTCTCT 630  
 DB 586 CTACAGAAAGCCAGGCGGCTCTCCAAAGCTCTCCAAAGCTCTCCAAAGCTCTCCAAAGCTCTCT 645  
 QY 631 GGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACACTCAAGATCAGC 690  
 DB 646 GGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACACTCAAGATCAGC 705  
 QY 691 AGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTAC 750  
 DB 706 AGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTAC 765  
 QY 751 ACCTTCGAGGGGGGACCAAGCTGGAAATATAAAGAAAGAAAAA 792  
 DB 766 ACCTTCGAGGGGGGACCAAGCTGGAAATATAAAGAAAGAAAAA 807  
 RESULT 6  
 AAA92443  
 ID AAA92443 standard; DNA; 828 BP.  
 AC AAA92443;  
 XX 15-JAN-2001 (first entry)  
 DT Plasmid pscM2 MABU2-scFv nucleotide sequence SEQ ID NO:24.  
 XX Monoclonal antibody; MABU; IAP; integrin associated protein;  
 KW single stranded Fv; apoptosis; blood disease; leukaemia;  
 KW cytostatic; ds.  
 XX Mus sp.  
 OS W0200053634-A1.  
 PN 14-SEP-2000.  
 PD 10-MAR-2000; 2000WO-JP01458.  
 PF 10-MAR-1999; 99JP-0063557.  
 PR (CHUS ) CHUGAI SEIYAKU KK.  
 PA Fukushima N, Uno S;  
 PI WPI; 2000-587428/55.  
 XX P-PSDB; AAB23819.  
 XX Single stranded Fv antibody fragment inducing apoptosis in nucleated  
 PT blood cells having integrin associated protein for treatment of  
 PT leukemia -  
 XX  
 PS Example 5; Page 64-66; 73pp; Japanese.  
 CC The present invention describes a polypeptide containing the variable  
 CC region of the light chain of a monoclonal antibody, which induces  
 CC apoptosis in nucleated blood cells having integrin associate protein  
 CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;  
 CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents  
 CC for the treatment of blood disorders which contain the polypeptide.  
 CC The polypeptide can be used in the treatment of blood disorders such  
 CC as leukaemia. The present sequence encodes the protein sequence from

```
CC pscM2 MABL2-scFv, which is used in an example from the present
CC invention.
XX
XX
SQ Sequence 828 BP; 210 A; 199 C; 219 G; 200 T; 0 other;

Query Match      63.4%; Score 526.4; DB 21; Length 828;
Best Local Similarity 82.8%; Pred. No. 4.4e-139;
Matches 631; Conservative 0; Mismatches 116; Indels 15; Gaps 2;

2y 46 GCGCGCATTCCTCTTGGCGCGGTTCAACTGCACAGTCTTGGGCTGAGCTGGTGAGG 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 46 GCTGCCCAACAGCCATGGCGAGTCCAGCTGCACAGTCTGGACCTGAACCTGGAAG 105

2y 106 CTGGGGCTTCAGTGACGCTGTCTCTCAAGGCTTCGGGTACACATTTACTGACTATGA 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 106 CTGGGGCTTCAGTGAAGTGTCTCTCAAGGCTTCGGGTACACATTTACTGACTATGA 165

2y 166 ATACACTGGGTGAGGCAGACACCTGTGCATGGCTCGAATGGATTGGAGCTATTGATCT 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 166 ATTCACTGGGTGAAGCAGAGAGCCAGGCGAGGCTTTGAGTGGATTGGATATATTATCT 225

2y 226 GAAACTGGTGGTACTGCTACAATCAGAAGTTCAAGCACAAGGCCATAGTACTGTAGAC 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 226 TACAATGATGGTACTAAGTATATAGAGAGTTCAAGCACAAGGCCACTGTGACTTCAGAC 285

2y 286 AAATCTCCAGCAGCCTACATGGAGCTCCGAGCTCGACATCTGAAGACTCTGCCGTC 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 286 AAATCTCCAGCAGCCTACATGGAGCTCCGAGCTCGACATCTGAAGACTCTGCCGTC 345

2y 346 TATTACTATACAAGATGG-----TTTGAGACTGGGGCCAAAGGACTCTGGTCT 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 346 TATTACTGTCAAGAGGGGTTACTATCTTACGACACTGGGGCCAAAGGACCACACTCTC 405

2y 394 ACTGTCTCTGCA--GAGGTAAATCCTCAGGATCTGGCTCCGAATCCAAACCCGGGAT 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 406 ACAGTCTCTCAGGTGGTGGTTCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 465

2y 451 GTTGATGATCAACCCCAACCTCTCCCTCCCTGTCAGTCTTGGAGATCAAGCTCCATC 510
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 466 GTTGATGATCAACCCCAACCTCTCCCTCCCTGTCAGTCTTGGAGATCAAGCTCCATC 525

2y 511 TCTGAGATCTAGTCAGAGCCCTTTTACACAGTAAATGGAATCACCTATTATATGGTAC 570
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 526 TCTTGAGATCAAGTCAGAGCCCTTGGCAGAGTAAATGGAAGACCTATTATATGGTAC 585

2y 571 CTGAGAAGCCAGGCGAGTCTCAAAAGCTCCTGATCTCAAAAGTTTCCAAACCGATTTC 630
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 586 CTGAGAAGCCAGGCGAGTCTCAAAAGCTCCTGATCTCAAAAGTTTCCAAACCGATTTC 645

2y 631 GGGTCCCAGACAGGTTTCAGTGGCAGTCAAGGACAGATTTACACTCAAGATCAGC 690
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 646 GGGTCCCAGACAGGTTTCAGTGGCAGTCAAGGACAGATTTACACTCAAGATCAGC 705

2y 691 AGAGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAAAGTACACATGTTCCGTAC 750
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 706 AGAGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAAAGTACACATGTTCCGTAC 765

2y 751 ACCTTCGGAGGGGGGACCAAGCTGGAATATAAAGAGAAAGAA 792
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
yb 766 ACCTTCGGAGGGGGGACCAAGCTGGAATATAAAGACTACAA 807
```

```
RESULT 7
AAH78148
D AAH78148 standard; DNA; 828 BP.
X
X AAH78148;
X
X 26-NOV-2001 (first entry)
X
X Nucleotide sequence of a murine antibody L chain.
X
X Apoptosis; nucleated blood cell; integrin-associated protein; IAP;
```

```
KW erythrocyte agglutination; blood disease; leukemia; myeloma;
KW Hodgkin's disease; non-Hodgkin's lymphoma; ss.
OS Mus sp.
XX
XX Key Location/Qualifiers
FH 1..825
FT CDS /tag= a
FT /product= "L chain"
XX
XX WO200166737-A1.
XX 13-SEP-2001.
XX 12-MAR-2001; 2001WO-JP01912.
XX 10-MAR-2000; 2000US-0523095.
XX 17-APR-2000; 2000JP-0115246.
XX 20-OCT-2000; 2000JP-0321822.
XX (CHUS) CHUGAI SEIVAKU KK.
XX Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;
XX WPI; 2001-570772/64.
XX P-PSDB; AAG67495.
XX
XX Reconstituted polypeptide induces apoptosis in nucleated blood cells
XX that contain integrin-associated protein (IAP), is useful for the
XX treatment of blood diseases such as leukemia.
XX
XX Example 5; Page 113-115; 141pp; Japanese.
XX
XX The specification describes a reconstituted polypeptide, which
XX induces apoptosis in nucleated blood cells that contain
XX integrin-associated protein (IAP). The polypeptide binds to IAP
XX without causing agglutination of erythrocytes. The polypeptide
XX contains at least two H chain V domains and at least two L chain
XX V domains of a monoclonal antibody which induces apoptosis in
XX nuclear blood cells having IAP. The reconstituted polypeptide is used
XX for the treatment of blood diseases such as acute or chronic myeloid
XX leukemia, acute or chronic lymphoid leukemia, adult T-cell leukemia,
XX multiple myeloma, mixed leukemia, hairy cell leukemia, Hodgkin's
XX disease or non-Hodgkin's lymphoma. The present sequence encodes a
XX murine monoclonal antibody L chain, which is used in the course of
XX the invention.
XX
XX Sequence 828 BP; 210 A; 199 C; 219 G; 200 T; 0 other;
```

```
Query Match      63.4%; Score 526.4; DB 22; Length 828;
Best Local Similarity 82.8%; Pred. No. 4.4e-139;
Matches 631; Conservative 0; Mismatches 116; Indels 15; Gaps 2;

Qy 46 GCGCGCATTCCTCTTGGCGCGGTTCAACTGCACAGTCTTGGGCTGAGCTGGTGAGG 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 46 GCTGCCCAACAGCCATGGCGAGTCCAGCTGCACAGTCTGGACCTGGAACCTGTAAG 105

Qy 106 CTGGGGCTTCAGTGACGCTGTCTCTCAAGGCTTCGGGCTACACATTTACTGACTATGA 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 106 CTGGGGCTTCAGTGAAGATGTCTCTCAAGGCTTCGGTATACACCTTCGCTAACCATGT 165

Qy 166 ATACACTGGGTGAGGCAGACACCTGTGTCATGGCTCGGCTTGGAGCTATTGATCCT 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 166 ATCACTGGGTGAAGCAGAGCCAGGCGGCTTCAGTGGATTGGATATATTATCT 225

Qy 226 GAAACTGGTGGTACTGCTTACAATCAGAAGTTCAAGCACAAGGCCATAGTACTGTAGAC 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 226 TACAATGATGGTACTAAGTATAATCAGAAGTTCAAGCACAAGGCCACTCTGACTTCAGAC 285

Qy 286 AAATCTCCAGCAGCCTACATGGAGCTCCGAGCTCGACATCTGAAGACTCTGCCGTC 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 286 AAATCTCCAGCAGCCTACATGGAGCTCCGAGCTCGACATCTGAAGACTCTGCCGTC 345
```

346 TATTACTATACAGATGG-----TTTGAGGACTGGGGCCAAAGGACTCTCGTC 393  
 346 TATTACTGTGCAAGAGGGGTTACTATATCTTACGACTGGGGCCAAAGGACTCTC 405  
 394 ACTGCTCTGCA---GAGGGTAAATCTCTAGGATCTGGCTCCGAATCCAAACCGGGAT 450  
 406 ACAGTCTCTCAGTGTGGTGGTTCGGGTGGTGGTTCGGGTGGTGGGATCGGAT 465  
 451 GTTGTGATGACCCCAACCCACTCTCCCTGCTCTCAGTCTTGGAGATCAAGCTCCATC 510  
 466 GTTGTGATGACCCCAACCCACTCTCCCTGCTCTCAGTCTTGGAGATCAAGCTCCATC 525  
 511 TCTTGCAGATCTAGTCAGAGCCTTTTACAGATTAATGGAATCACCTATTACATGGTAC 570  
 526 TCTTGCAGATCAAGTCAGAGCCTTTGTCACAGTAAATGGAAGACCTATTACATGGTAC 585  
 571 CTGCAGAAAGCCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTCT 630  
 586 CTGCAGAAAGCCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTCT 645  
 631 GGGTCCCGACAGAGTTTCAGTGGCAGTGGATCAGGAGAGATTTTACACTCAAGATCAGC 690  
 646 GGGTCCCGACAGAGTTTCAGTGGCAGTGGATCAGTACAGATTTTACACTCATGATCAGC 705  
 691 AGAGTGGAGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTAC 750  
 706 AGAGTGGAGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTAC 765  
 751 ACCTTCGGAGGGGGGACCAAGCTCGAAATAAAGCAAGAAAA 792  
 766 ACCTTCGGAGGGGGGACCAAGCTCGAAATAAAGCAACTACAA 807

## RESULT 8

ABK71327  
 ID ABK71327 standard; DNA; 828 BP.  
 AC ABK71327;  
 XX 30-JUL-2002 (first entry)  
 DE DNA encoding thrombopoietin agonist antibody associated protein #7.  
 XX Modified antibody; thrombopoietin; TPO; agonist;  
 KW TPO receptor; platelet reduction-associated blood disease;  
 KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;  
 KW gene; ds.  
 XX Mus sp.  
 OS  
 XX WO200233072-A1.  
 XX PD 25-APR-2002.  
 XX PF 22-OCT-2001; 2001WO-JP09259.  
 XX PR 20-OCT-2000; 2000JP-0321821.  
 XX PR 17-APR-2001; 2001WO-JP03288.  
 XX PR 12-SEP-2001; 2001JP-0277314.  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;  
 PI WPI: 2002-383513/41.  
 XX DR P-PSDB; ABG35313.  
 XX PT Degraded thrombopoietin agonist antibodies containing H and L chain V  
 PT domains of monoclonal antibody, useful in preventives and/or remedies  
 PT for blood diseases, thrombocytopenia following cancer chemotherapy or  
 XX leukaemia  
 XX Example 5; Page 152-154; 213pp; Japanese.

XX The invention describes a modified antibody comprising at least 2 heavy  
 CC chain variable domains and 2 or more light chain variable domains of an  
 CC antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing  
 CC the TPO receptor to crosslink. The antibodies are useful in preventives  
 CC and/or remedies for platelet reduction-associated blood diseases,  
 CC thrombocytopenia following cancer chemotherapy or leukaemia. The  
 CC antibody can act as a TPO signal transduction agonist by transducing a  
 CC signal into cells by crosslinking a TPO receptor to exert TPO agonism.  
 CC This sequence encodes a thrombopoietin (TPO) agonist antibody associated  
 CC protein.

XX Sequence 828 BP; 210 A; 199 C; 219 G; 200 T; 0 other;

Query Match 63.4%; Score 526.4; DB 24; Length 828;  
 Best Local Similarity 82.8%; Pred. No. 4.4e-139;  
 Matches 631; Conservative 0; Mismatches 116; Indels 15; Gaps 2;

QY 46 GCGGCGCATTCGCCCTTTGGCGGGTTCAACTGCAGCAGTCTGGGGCTGAGCTGTGAGG 105  
 DB 46 GCTGCCCCAACCAAGCCATGGCGCAGGTCCAGCTGCAGCAGTCTGGACTGAACCTGGTAAAG 105  
 QY 106 CCTGGGGCTTCAGTGACGCTGCTCTGCAAGGCTTCGGGCTTACACATTTACTGACTATGAA 165  
 DB 106 CTTGGGGCTTCAGTGAAGATGCTCTGCAAGGCTTCGGATACACCTTCGCTAACCATGTT 165  
 QY 166 ATACACTGGGTGAGGCGAGACACCTGTGCATGGCTCGAATGGATTGGAGCTATTGATCTCT 225  
 DB 166 ATTCACTGGGTGAAGCAGAAAGCCAGGCGAGGCTTGGTGGATTGGATATATTTATCTCT 225  
 QY 226 GAAACTGGTGTACTGCTTACATCAGAGTTCAGGACCAAGGCCATAGTACTGTAGAC 285  
 DB 226 TACAATGATGGTACTAAGTATATATGAAAGTTCAAGGACAAGGCCACTCTGACTTCAGAC 285  
 QY 286 AAATCTCTCAGCAGACGCTACATGAGCTCCGAGCTGCAGCTGACATCTGAAGACTCTGCCGTC 345  
 DB 286 AAATCTCTCAGCAGACGCTACATGAGCTTCAGGCTGAGGCTGCGCTCTGAGGACTCTGCCGTC 345  
 QY 346 TATTACTATACAAGATGG-----TTTGAGGACTGGGGCCAAAGGACTCTGGTC 393  
 DB 346 TATTACTGTCAAGAGGGGTTACTATCTTACGACGACTGGGGCCAAAGCACCACCTCTC 405  
 QY 394 ACTGCTCTGCA---GAGGGTAAATCTCTAGGATCTGGCTCCGAATCCAAACCGGGGAT 450  
 DB 406 ACAGTCTCTCAGTGTGGTGGTTCGGGTGGTGGTGGTTCGGGTGGTGGGATCGGAT 465  
 QY 451 GTTGTGATGACCCCAACCCACTCTCCCTGCTCTCAGTCTTGGAGATCAAGCTCCATC 510  
 DB 466 GTTGTGATGACCCCAACCCACTCTCCCTGCTCTCAGTCTTGGAGATCAAGCTCCATC 525  
 QY 511 TCTTGCAGATCTAGTCAGAGCCTTTTACAGATTAATGGAATCACCTATTATTTACATGGTAC 570  
 DB 526 TCTTGCAGATCAAGTCAGAGCCTTTGTCACAGTAAATGGAAGACCTATTATTTACATGGTAC 585  
 QY 571 CTGCAGAAAGCCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTCT 630  
 DB 586 CTGCAGAAAGCCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTCT 645  
 QY 631 GGGTCCCGACAGAGTTTCAGTGGCAGTGGATCAGGAGAGATTTTACACTCAAGATCAGC 690  
 DB 646 GGGTCCCGACAGAGTTTCAGTGGCAGTGGATCAGTACAGATTTTACACTCATGATCAGC 705  
 QY 691 AGAGTGGAGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTAC 750  
 DB 706 AGAGTGGAGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTAC 765  
 QY 751 ACCTTCGGAGGGGGGACCAAGCTCGAAATAAAGCAAGAAAA 792  
 DB 766 ACCTTCGGAGGGGGGACCAAGCTCGAAATAAAGCAACTACAA 807

RESULT 9  
 ABA04524







QY 680 TCAAGATCAGCAGAGTGGAGGCTCAGGATCTGGAGTTTATTTCTGCTCTCAAGTACAC 739  
 |||||  
 Db 686 TCAAGATCAGCAGAGTGGAGGCTCAGGATCTGGAGTTTATTTCTGCTCTCAAGTACAC 745  
 |||||  
 QY 740 ATGTTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAGAGAAAAA 792  
 |||||  
 Db 746 ATGTTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAGAGTACAAA 798  
 |||||

## RESULT 13

ABAO4523  
 ID ABAO4523 standard; DNA; 819 BP.  
 XX  
 AC ABAO4523;  
 XX  
 DT 15-FEB-2002 (first entry)  
 XX  
 DE Murine MABL-1 #4 coding sequence.

XX Murine; cytostatic; antiinflammatory; antianaemic; vasotropic;  
 XX antibody; signal transduction; cancer; inflammation; hormonal disorder;  
 KW leukaemia; lymphoma; aplastic anaemia; skeletal malformation; ds.  
 XX  
 OS Mus sp.

XX Location/Qualifiers  
 FH 1..816  
 FT CDS  
 FT /\*tag= a  
 FT /product= "Murine MABL-1 #4"

XX WO200179494-A1.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-JP03288.

XX 17-APR-2000; 2000JP-0115246.

XX 20-OCT-2000; 2000JP-0321821.

XX 20-OCT-2000; 2000JP-0321822.

XX 12-MAR-2001; 2001WO-JP01912.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;

XX WPI; 2002-066368/09.

XX P-PSDB; AAM47632.

XX Antibodies for treatment of diseases associated with cell

XX proliferation, hormonal disorders and cytokines comprise agonist

XX activity to signal transduction across cell membranes -

XX Example 5; Page 129-131; 173pp; Japanese.

XX The present invention relates to modified antibodies. The antibodies  
 CC contain two or more H chain V domains and two or more L chain V domains  
 CC of a monoclonal antibody (MAB) which is capable of transmitting a signal  
 CC across the cell membrane by cross-linking a cell surface molecule, where  
 CC the antibodies can serve as signal transduction agonists. The antibodies  
 CC are useful for treatment and prevention of a broad range of disorders in  
 CC which signal transduction is implicated, such as cancer, inflammation,  
 CC hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and  
 CC skeletal malformations. The present sequence was used to illustrate the  
 CC present invention.

XX Sequence 819 BP; 208 A; 195 C; 223 G; 193 T; 0 other;

XX Query Match 62.8%; Score 521.4; DB 24; Length 819;

XX Best Local Similarity 81.8%; Pred. No. 1.1e-137;

XX Matches 632; Conservative 0; Mismatches 126; Indels 15; Gaps 2;

XX 35 TTTTGGCGGGCGGCGCATCTGCTTTGGCGGGTTCAACTGCAGCAGTCTGGGGCTG 94

Db 26 TCTTGTAGCAACAGCTACAGGTGTGCACTCCAGTCCAGCTGCAGCAGTCTGGACCTG 85  
 |||||  
 QY 95 AGCTGTGAGGCTCGGGCTTCAGTGACGCTGTCTGCAAGGCTTCGGGCTACACATTTA 154  
 |||||  
 Db 86 ACCTGTAAAGCTCGGGCTTCAGTGAAGATGTCTGCAAGGCTTCGGATACACCTTCG 145  
 |||||  
 QY 155 CTGACTATGAATACACTGGGTGAGGCAGACACCTGTGATGCGCTGGAAATGGATTGGAG 214  
 |||||  
 Db 146 TTAACCATGTTATGCACCTGGGTGAAGCAAGCCAGGCGGCTTGAATGGATTGGAT 205  
 |||||  
 QY 215 CTATTGATCTGAAACTGGGTGCTTACCAATCAGAAAGTTCAAGGCAAGGCCATAG 274  
 |||||  
 Db 206 ATATTATCTTACAATGATGGTAACTAAGTACAATGAGAAGTTCAAGGCAAGGCCACAC 265  
 |||||  
 QY 275 TGAAGTGAACAAATCTCCAGCAGCCTTACATGAGCTCCGAGCTGACATCTGAAG 334  
 |||||  
 Db 266 TGAAGTGAACAAATCTCCAGCAGCCTTACATGAGCTCAGCAGCTGGCCTCTGAGG 325  
 |||||  
 QY 335 ACTCTGCGTCTTACTACTACAGATGG-----TTTGAGGACTGGGGCAAG 382  
 |||||  
 Db 326 ACTCTGCGTCTTACTACTGTGCAAGAGGGGTTTACTATAGTTACGACGACTGGGGCAAG 385  
 |||||  
 QY 383 GGAAGTCTGCTGCTCTGCA---GAGGGTAAATCCTCAGGATCTGGCTCCGAATCCA 439  
 |||||  
 Db 386 GCACCACTCTCAGAGTCTCTCAGGTGGTGGTTCGGGTGGTGGTTCGGGTGGT 445  
 |||||  
 QY 440 AACCCGGGATGTTGTGATGACCCCAAAACCCACTCTCCCTGCTGCTGCTGAGATC 499  
 |||||  
 Db 446 GCGGATCGGATGTTGTGATGACCCCAAACTCCACTCTCCCTGCTGCTGAGATC 505  
 |||||  
 QY 500 AAGCCTCCATCTCTGAGATCTAGTCAGAGCCTTTTACACAGTAATGGAATCACCTATT 559  
 |||||  
 Db 506 AAGCCTCCATCTCTGAGATCTAGTCAGAGCCTTTTACACAGTAATGGAATCACCTATT 565  
 |||||  
 QY 560 TACATGTTGTTACCTGCAAGAGCCAGGCTCTCCAAAGCTCTGATCTACAAAGTTTCCA 619  
 |||||  
 Db 566 TACAATGGTACCTTACAGAGCCAGGCTCTCCAAAGCTCTGATCTACAAAGTTTCCA 625  
 |||||  
 QY 620 ACCGATTTTCTGGGGTCCCAGACAGGTTTCAAGTGGCAGTGGATCAGGACAGATTTCACAC 679  
 |||||  
 Db 626 ACCGATTTTCTGGGGTCCCAGACAGGTTTCAAGTGGCAGTGGATCAGGACAGATTTCACAC 685  
 |||||  
 QY 680 TCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACAC 739  
 |||||  
 Db 686 TCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACAC 745  
 |||||  
 QY 740 ATGTTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAGAGAAAAA 792  
 |||||  
 Db 746 ATGTTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAGAGTACAAA 798  
 |||||

## RESULT 14

AA92444

ID AAA92444 standard; DNA; 819 BP.

XX AC AAA92444;

XX DT 15-JAN-2001 (first entry)

XX DE Plasmid pCHOM2 MABL2-scFv nucleotide sequence SEQ ID NO:25.

XX KW Monoclonal antibody; MABL; IAP; integrin associated protein;

XX KW single stranded Fv; apoptosis; blood disease; leukaemia;

XX KW cytostatic; ds.

XX OS Mus sp.

XX PN WO200053634-A1.

XX PD 14-SEP-2000.

XX PF 10-MAR-2000; 2000WO-JP01458.









GenCore version 5.1.4.p5.4578  
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DM protein - protein search, using sw model

Run on: May 16, 2003, 14:18:25 ; Search time 76 Seconds  
(without alignments)  
471.637 Million cell updates/sec

Title: US-09-358-321C-32

Perfect score: 1391

Sequence: 1 MVSAILVYLLAAAHSAFA.....FGGKLEIKKEKLISEDL 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	1391	100.0	269	21	AA68992
2	990	71.2	267	21	AA689776
3	984.5	70.8	274	21	AA6823819
4	984.5	70.8	274	22	AA687495
5	984.5	70.8	274	23	AA6835113
6	984.5	70.8	274	23	AA687633
7	978.5	70.3	271	21	AA6823820
8	978.5	70.3	271	22	AA687496
9	978.5	70.3	271	23	AA6835114
10	978.5	70.3	271	23	AA687634

11	973.5	70.0	533	22	AA687499	Amino acid sequenc
12	973.5	70.0	533	23	AA6835117	Thrombopoietin ago
13	973.5	70.0	533	23	AA6876337	Murine MABL-2 #6.
14	963.5	69.3	274	21	AA6823817	Plasmid pscM1 MABL
15	963.5	69.3	274	22	AA687493	Amino acid sequenc
16	963.5	69.3	274	23	AA6835111	Thrombopoietin ago
17	963.5	69.3	274	23	AA687631	Murine MABL-1 #3
18	959.5	69.0	245	22	AA687498	Amino acid sequenc
19	959.5	69.0	245	23	AA6835116	Thrombopoietin ago
20	959.5	69.0	245	23	AA687636	Murine MABL-2 #5.
21	957.5	68.8	271	21	AA6823818	Plasmid pCHOM1 MAB
22	957.5	68.8	271	22	AA687494	Amino acid sequenc
23	957.5	68.8	271	23	AA6835112	Thrombopoietin ago
24	957.5	68.8	271	23	AA687632	Murine MABL-1 #4.
25	952	68.4	256	22	AA687500	Amino acid sequenc
26	952	68.4	256	23	AA6835118	Thrombopoietin ago
27	952	68.4	256	23	AA687638	Murine MABL-2 #7.
28	944	67.9	532	21	AA6878328	Bispecific anti-ze
29	943.5	67.8	251	20	AA6817958	Mouse scfV fragmen
30	943.5	67.8	251	20	AA6817962	Mouse scfV fragmen
31	943.5	67.8	507	23	AA6872858	8G7C10x4-7 bispeci
32	943.5	67.8	510	23	AA6872859	6E5A7x4-7 bispeci
33	943.5	67.8	510	23	AA6872860	Human p53 tetramer
34	927.5	66.7	252	17	AA6802279	26-10 anti-digoxin
35	927.5	66.7	252	19	AA6853169	26-10 anti-digoxin
36	927.5	66.7	252	20	AA680423	Anti-digoxin srfv
37	925.5	66.5	367	13	AA6827244	Sequence encoded b
38	923.5	66.4	249	9	AA680154	Biosynthetic antib
39	922.5	66.3	246	13	AA6827245	Sequence of the AA
40	914.5	65.7	311	11	AA6805378	Multifunctional pr
41	914.5	65.7	313	22	AA6862305	Single chain antib
42	910.5	65.5	246	14	AA6844229	Chimeric Ig superf
43	906.5	65.2	311	9	AA680151	Multifunctional pr
44	890	64.0	251	22	AA6870171	Recombinant antibo
45	889	63.9	261	14	AA6844230	Chimeric Ig superf

#### ALIGNMENTS

#### RESULT 1

AA68992

ID AA68992 standard; Protein; 269 AA.

XX AA68992;

XX AA68992;

DT 30-MAY-2000 (first entry)

DE Amino acid sequence of a single chain anti-delta9-desaturase antibody.

XX Delta9-desaturase; antibody; transit peptide; passenger protein;

KW plant cell organelle; maize; stearyl-ACP-delta9-desaturase;

KW transgenic plant.

XX Synthetic.

OS Mus sp.

XX Key

FT Protein

FT Location/Qualifiers

FT 21..269

FT /note= "mature protein"

XX WO200005391-A1.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-US16405.

XX 21-JUL-1998; 98US-0093587.

XX (DOWC) DOW AGROSCIENCES LLC.

XX Sukhapinda K, Hasler JM, Petell JK, Strickland JA, Folkerts O;

XX



```

XX KW Monoclonal antibody; MABL; IAP; integrin associated protein;
XX KW single stranded Fv; apoptosis; blood disease; leukaemia;
XX KW cytostatic.
XX OS Mus sp.
XX WO200053634-A1.
XX PN
XX PD 14-SEP-2000.
XX PF 10-MAR-2000; 2000WO-JP01458.
XX PR 10-MAR-1999; 99JP-0063557.
XX (CHUS ) CHUGAI SEIYAKU KK.
XX PA Fukushima N, Uno S;
XX PI WPI; 2000-587428/55.
XX DR N-PSDB; AAA92443.
XX PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
XX PT blood cells having integrin associated protein for treatment of
XX PT leukemia
XX
XX Example 5; Page 64-66; 73pp; Japanese.
XX
XX The present invention describes a polypeptide containing the variable
XX region of the light chain of a monoclonal antibody, which induces
XX apoptosis in nucleated blood cells having integrin associate protein
XX (IAP). Also described are: (1) DNA encoding the novel polypeptide;
XX (2) animal or microbial cells expressing the DNA of (1); and (3) agents
XX for the treatment of blood disorders which contain the polypeptide.
XX The polypeptide can be used in the treatment of blood disorders such
XX as leukaemia. The present sequence represents the protein sequence from
XX pscM2 MABL2-scfV, which is used in an example from the present
XX invention.
XX
XX Sequence 274 AA;
XX
Query Match 70.8%; Score 984.5; DB 21; Length 274;
Best Local Similarity 76.0%; Pred. NO. 1.1e-68;
Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2;

QY 10 LLAARHSAFAAVALQOQSGAEIVRPGASVTLSCKASGYTFTDYEIHWVROTPTVHGLEWIG 69
DB 12 LLLAQAQPAQAQVLOQSGPELVKPGASVNRKSKASGYTFANHHVHWKQKPGGLEWIG 71

QY 70 AIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRSLTSEDSAVYYTR----WFDWQG 125
DB 72 YIYPNDGTKYNEKFKDKATLTSKSTTAYMDLSSLAEDSAVYYCARGYYTYDDWQG 131

QY 126 GTLVTVSAEGKSSGSGSESKPG-DVWMTNPNPLSPVSLGDAQSISCRSSSLLHNSGITY 184
DB 132 GTTLTVSSGGGGGGGGGGGGDVWMTQSPSLPVLGDAQSISCRSSSLSVHNSGITY 191

QY 185 LHWYLOKPGQSPKLLIYKVSNRFSGVDRFSGSGCTDFTLKISRVEADLGVYFCQSOST 244
DB 192 LHWYLOKPGQSPKLLIYKVSNRFSGVDRFSGSGSVTDFTLMTISRVEADLGVYFCQSOST 251

QY 245 HVPYTFGGGTGLEIKEEK 262
DB 252 HVPYTFGGGTGLEIKDYK 269

RESULT 4
AAG67495
ID AAG67495 standard; Protein; 274 AA.
XX
AC AAG67495;
XX
DT 26-NOV-2001 (first entry)

```

```

XX DE Amino acid sequence of a murine antibody L chain.
XX KW Apoptosis; nucleated blood cell; integrin-associated protein; IAP;
XX KW erythrocyte agglutination; blood disease; leukemia; myeloma;
XX KW Hodgkin's disease; non-Hodgkin's lymphoma.
XX OS Mus sp.
XX WO200166737-A1.
XX PN
XX PD 13-SEP-2001.
XX PF 12-MAR-2001; 2001WO-JP01912.
XX PR 10-MAR-2000; 2000US-0523095.
XX PR 17-APR-2000; 2000JP-0115246.
XX PR 20-OCT-2000; 2000JP-0321822.
XX (CHUS ) CHUGAI SEIYAKU KK.
XX PA Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;
XX PI WPI; 2001-570772/64.
XX DR N-PSDB; AAH78148.
XX
XX Reconstituted polypeptide induces apoptosis in nucleated blood cells
XX PT that contain integrin-associated protein (IAP), is useful for the
XX PT treatment of blood diseases such as leukemia
XX
XX Example 5; Page 113-115; 141pp; Japanese.
XX
XX The specification describes a reconstituted polypeptide, which
XX induces apoptosis in nucleated blood cells that contain
XX integrin-associated protein (IAP). The polypeptide binds to IAP
XX without causing agglutination of erythrocytes. The polypeptide
XX contains at least two H chain V domains and at least two L chain
XX V domains of a monoclonal antibody which induces apoptosis in
XX nuclear blood cells having IAP. The reconstituted polypeptide is used
XX for the treatment of blood diseases such as acute or chronic myeloid
XX leukemia, acute or chronic lymphoid leukemia, adult T-cell leukemia,
XX multiple myeloma, mixed leukemia, hairy cell leukemia, Hodgkin's
XX disease or non-Hodgkin's lymphoma. The present sequence represents a
XX CC a murine monoclonal antibody L chain, which is used in the course of
XX CC the invention.
XX
XX Sequence 274 AA;
XX
Query Match 70.8%; Score 984.5; DB 22; Length 274;
Best Local Similarity 76.0%; Pred. NO. 1.1e-68;
Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2;

QY 10 LLAARHSAFAAVALQOQSGAEIVRPGASVTLSCKASGYTFTDYEIHWVROTPTVHGLEWIG 69
DB 12 LLLAQAQPAQAQVLOQSGPELVKPGASVNRKSKASGYTFANHHVHWKQKPGGLEWIG 71

QY 70 AIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRSLTSEDSAVYYTR----WFDWQG 125
DB 72 YIYPNDGTKYNEKFKDKATLTSKSTTAYMDLSSLAEDSAVYYCARGYYTYDDWQG 131

QY 126 GTLVTVSAEGKSSGSGSESKPG-DVWMTNPNPLSPVSLGDAQSISCRSSSLLHNSGITY 184
DB 132 GTTLTVSSGGGGGGGGGGGGDVWMTQSPSLPVLGDAQSISCRSSSLSVHNSGITY 191

QY 185 LHWYLOKPGQSPKLLIYKVSNRFSGVDRFSGSGCTDFTLKISRVEADLGVYFCQSOST 244
DB 192 LHWYLOKPGQSPKLLIYKVSNRFSGVDRFSGSGSVTDFTLMTISRVEADLGVYFCQSOST 251

QY 245 HVPYTFGGGTGLEIKEEK 262
DB 252 HVPYTFGGGTGLEIKDYK 269

```

```
RESULT 5
ABG35313
ID ABG35313 standard; Protein; 274 AA.
XX
XX ABG35313;
AC
XX
XX 30-JUL-2002 (first entry)
IDT
XX
XX Thrombopoietin agonist antibody associated protein #7.
XX
XX Modified antibody; thrombopoietin; TPO; agonist;
XX DE
XX TPO receptor; platelet reduction-associated blood disease;
XX KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.
XX
XX Mus sp.
XX
XX OS
XX
XX WO200233072-A1.
XX
XX 25-APR-2002.
PD
XX
XX 22-OCT-2001; 2001WO-JP09259.
XX
XX 20-OCT-2000; 2000JP-0321821.
XX
XX 17-APR-2001; 2001WO-JP03288.
XX
XX 12-SEP-2001; 2001JP-0277314.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;
PI
XX WPI; 2002-383513/41.
XX
XX N-PSDB; ABK71327.
XX
XX Degraded thrombopoietin agonist antibodies containing H and L chain V
XX domains of monoclonal antibody, useful in preventives and/or remedies
XX for blood diseases, thrombocytopenia following cancer chemotherapy or
XX leukaemia -
XX
XX Disclosure; Page 152-154; 213pp; Japanese.
XX
XX The invention describes a modified antibody comprising at least 2 heavy
XX chain variable domains and 2 or more light chain variable domains of an
XX antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
XX the TPO receptor to crosslink. The antibodies are useful in preventives
XX and/or remedies for platelet reduction-associated blood diseases.
XX CC thrombocytopenia following cancer chemotherapy or leukaemia. The
XX antibody can act as a TPO signal transduction agonist by transducing a
XX signal into cells by crosslinking a TPO receptor to exert TPO agonism.
XX This is the amino acid sequence of a thrombopoietin (TPO) agonist
XX antibody associated protein.
XX
XX Sequence 274 AA;
XX
XX Query Match 70.8%; Score 984.5; DB 23; Length 274;
XX Best Local Similarity 76.0%; Pred. No. 1.1e-68;
XX Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2;
XX
QY 10 LLA AAAHSAFAA VQLOQSGAE LVRPGASVTLSCKASGYTFDTY EIHVWROT PVHGLEWIG 69
DB 12 LLL LLAQA PMAQVQLOQSGPELVKPGASVKMSCKASGYTFANHV IHWVKRPGQGLEWIG 71
QY 70 AIDPETGGTAYNOKFKDKAI VTDKSSSTAYMELRSLTSEDSAVYYTTR ---WFDWQ 125
DB 72 YIYPNDGT KYNEKFKDKATLTSDKSSSTAYMDLSSLAS EDSAVYYCARGGYTYDDWQ 131
QY 126 GTLVTVSAEGKSSGSGSESKPG -DVVMTPNPLSLPVSLG DQASISCRSSQSLHNSGITY 184
DB 132 GTTLTVSSGGGGGGGGGGGSDVVMVTQSP LSLPVSLG DQASISCRSSQSLVHNSGITY 191
QY 185 LHWYLOKPGOSP KLLIYKYVSNRFGVPDRFSGSGGTDTFTL KISRVEAEDLG VYFCQST 244
DB 192 LHWYLOKPGOSP KLLIYKYVSNRFGVPDRFSGSGGTDTFTL KISRVEAEDLG VYFCQST 251

RESULT 6
AAM47633
ID AAM47633 standard; Protein; 274 AA.
XX
XX AAM47633;
AC
XX
XX 15-FEB-2002 (first entry)
DT
XX
XX Murine MABL-2 #3.
DE
XX
XX Murine; cytostatic; antiinflammatory; antianaemic; vasotropic;
XX antibody; signal transduction; cancer; inflammation; hormonal disorder;
XX leukaemia; lymphoma; aplastic anaemia; skeletal malformation.
XX
XX Mus sp.
XX
XX WO200179494-A1.
XX
XX 25-OCT-2001.
PD
XX
XX 17-APR-2001; 2001WO-JP03288.
XX
XX 17-APR-2000; 2000JP-0115246.
XX
XX 20-OCT-2000; 2000JP-0321821.
XX
XX 20-OCT-2000; 2000JP-0321822.
XX
XX 12-MAR-2001; 2001WO-JP01912.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;
PI
XX WPI; 2002-066368/09.
XX
XX N-PSDB; ABA04524.
XX
XX Antibodies for treatment of diseases associated with cell
XX proliferation, hormonal disorders and cytokines comprise agonist
XX activity to signal transmission across cell membranes -
XX
XX Disclosure; Page 131-133; 173pp; Japanese.
XX
XX The present invention relates to modified antibodies. The antibodies
XX contain two or more H chain V domains and two or more L chain V domains
XX of a monoclonal antibody (MAB) which is capable of transmitting a signal
XX across the cell membrane by cross-linking a cell surface molecule, where
XX the antibodies can serve as signal transmission agonists. The antibodies
XX are useful for treatment and prevention of a broad range of disorders in
XX which signal transduction is implicated, such as cancer, inflammation,
XX hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and
XX skeletal malformations. The present sequence was used to illustrate the
XX present invention.
XX
XX Sequence 274 AA;
XX
XX Query Match 70.8%; Score 984.5; DB 23; Length 274;
XX Best Local Similarity 76.0%; Pred. No. 1.1e-68;
XX Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2;
XX
QY 10 LLA AAAHSAFAA VQLOQSGAE LVRPGASVTLSCKASGYTFDTY EIHVWROT PVHGLEWIG 69
DB 12 LLL LLAQA PMAQVQLOQSGPELVKPGASVKMSCKASGYTFANHV IHWVKRPGQGLEWIG 71
QY 70 AIDPETGGTAYNOKFKDKAI VTDKSSSTAYMELRSLTSEDSAVYYTTR ---WFDWQ 125
DB 72 YIYPNDGT KYNEKFKDKATLTSDKSSSTAYMDLSSLAS EDSAVYYCARGGYTYDDWQ 131
QY 126 GTLVTVSAEGKSSGSGSESKPG -DVVMTPNPLSLPVSLG DQASISCRSSQSLHNSGITY 184
DB 132 GTTLTVSSGGGGGGGGGGGSDVVMVTQSP LSLPVSLG DQASISCRSSQSLVHNSGITY 191
QY 185 LHWYLOKPGOSP KLLIYKYVSNRFGVPDRFSGSGGTDTFTL KISRVEAEDLG VYFCQST 244
DB 192 LHWYLOKPGOSP KLLIYKYVSNRFGVPDRFSGSGGTDTFTL KISRVEAEDLG VYFCQST 251
```

Qy	185	LHWYQKPGQSPKLLIYKVNRSFGVPDRFSGSGSTDTFLKISRVEADLGVYFCQSQT	244
Db	192	LHWYQKPGQSPKLLIYKVNRSFGVPDRFSGSGVTDFLMISRVEADLGVYFCQSQT	251
Qy	245	HPVYTFGGGTGLKLEIKK	262
Db	252	HPVYTFGGGTGLKLEIKDYK	269

AA023820	ID	AA023820 standard; Protein; 271 AA.
XX	AC	
XX	AC	AA023820;
XX	DT	
XX	DT	15-JAN-2001 (first entry)
XX	DE	
XX	DE	Plasmid pCHOM2 MABL2-scfV protein sequence SEQ ID NO:25.
XX	KW	Monoclonal antibody; MABL; IAP; integrin associated protein;
KW	KW	single stranded Fv; apoptosis; blood disease; leukaemia;
KW	KW	cytostatic.
XX	OS	
XX	OS	Mus sp.
XX	PN	WO200053634-A1.
XX	PN	
XX	PD	14-SEP-2000.
XX	PF	
XX	PF	10-MAR-2000; 2000WO-JP01458.
XX	PR	
XX	PR	10-MAR-1999; 99JP-0063557.
XX	PA	(CHUS ) CHUGAI SEIYAKU KK.
XX	PI	
XX	PI	Fukushima N, Uno S;
XX	XX	
XX	DR	WPI; 2000-587428/55.
XX	DR	N-PSDB; AAA92444.
XX	XX	
XX	PT	Single stranded Fv antibody fragment inducing apoptosis in nucleated
PT	PT	blood cells having integrin associated protein for treatment of
PT	PT	leukemia
XX	PS	
XX	PS	Example 5; Page 66-68; 73pp; Japanese.

CC (2) animal or microbial cells expressing the DNA of (1); and (3) agent  
CC for the treatment of blood disorders which contain the polypeptide.  
CC The polypeptide can be used in the treatment of blood disorders such  
CC as leukaemia. The present sequence represents the protein sequence fr  
CC c pCHOM2 MABL2-scFv, which is used in an example from the present  
CC invention.  
XX  
SQ Sequence 271 AA;  
  
Query Match 70.3%; Score 978.5; DB 21; Length 271;  
Best Local Similarity 74.0%; Pred. No. 3.2e-68;  
Matches 196; Conservative 19; Mismatches 43; Indels 7; Gaps

[illegible]

Db 4 SCILF--LVATATGVDVSOVLOQSGPELVKPGASVKMSCKASGYTFANHVIHWKQPG 61  
 QY 63 HGLEWICAIIDPETGCTAYNOKFKDKATVTDKSSSTAYMELRSLTSDSAVYYVTR---- 118  
 Db 62 QGLEWIGYIYPNDGTYNEKFKDKATLTDKSSSTAYMDLSSLASDSAVYCARGGY 121  
 QY 119 WFEDWGQGTTLVTSVSAEGKSSGSGSESKPG-DVMTNPNPLSLPVSLGQDASISCRSSQSL 177  
 Db 122 TYDDWGQGTTLTVSSGGGGGGGGSDVMTQSPSLPVSLGQDASISCRSSQSLV 181  
 QY 178 HSNGITLHWYLOKPGSPKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGV 237  
 Db 182 HSNKGYTLHWYLOKPGSPKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGV 241  
 QY 238 YFCSQSTHVPYTFGGGKLEIKEEK 262  
 Db 242 YFCSQSTHVPYTFGGGKLEIKEEK 266  
 RESULT 9  
 ABG35314  
 ID ABG35314 standard; Protein; 271 AA.  
 XX AC ABG35314;  
 XX AC  
 XX DT 30-JUL-2002 (first entry)  
 XX DT  
 XX DT Thrombopoietin agonist antibody associated protein #8.  
 XX DT  
 XX DT Modified antibody; thrombopoietin; TPO; agonist;  
 KW TPO receptor; platelet reduction-associated blood disease;  
 KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.  
 KW  
 XX  
 XX Mus sp.  
 XX OS  
 XX XX  
 XX PN WO200233072-A1.  
 XX XX  
 XX PD 25-APR-2002.  
 XX XX  
 XX PF 22-OCT-2001; 2001WO-JP09259.  
 XX XX  
 XX PR 20-OCT-2000; 2000JP-0321821.  
 XX PR 17-APR-2001; 2001WO-JP03288.  
 XX PR 12-SEP-2001; 2001JP-0277314.  
 XX XX  
 XX PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX XX  
 XX TS Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;  
 XX WPI; 2002-383513/41.  
 XX DR N-PSDB; ABK71328.  
 XX DR  
 XX DR Degraded thrombopoietin agonist antibodies containing H and L chain V  
 PT domains of monoclonal antibody, useful in preventives and/or remedies  
 PT for blood diseases, thrombocytopenia following cancer chemotherapy or  
 PT leukaemia  
 XX  
 XX PS Disclosure; Page 154-156; 213pp; Japanese.  
 XX PS  
 XX CC The invention describes a modified antibody comprising at least 2 heavy  
 CC chain variable domains and 2 or more light chain variable domains of an  
 CC antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing  
 CC the TPO receptor to crosslink. The antibodies are useful in preventives  
 CC and/or remedies for platelet reduction-associated blood diseases,  
 CC thrombocytopenia following cancer chemotherapy or leukaemia. The  
 CC antibody can act as a TPO signal transduction agonist by transducing a  
 CC signal into cells by crosslinking a TPO receptor to exert TPO agonism.  
 CC This is the amino acid sequence of a thrombopoietin (TPO) agonist  
 CC antibody associated protein.  
 XX  
 XX Sequence 271 AA;  
 SQ

Query Match

70.3%; Score 978.5; DB 23; Length 271;

Best Local Similarity 74.0%; Pred. No. 3.2e-68;  
 Matches 196; Conservative 19; Mismatches 43; Indels 7; Gaps 3;  
 QY 3 SAIVLVLLAAAHSAFAAVOLOQSGAEIVRPGASVTLSCKASGYTFTDYEIHWKQTPV 62  
 Db 4 SCILF--LVATATGVDVSOVLOQSGPELVKPGASVKMSCKASGYTFANHVIHWKQPG 61  
 QY 63 HGLEWICAIIDPETGCTAYNOKFKDKATVTDKSSSTAYMELRSLTSDSAVYYVTR---- 118  
 Db 62 QGLEWIGYIYPNDGTYNEKFKDKATLTDKSSSTAYMDLSSLASDSAVYCARGGY 121  
 QY 119 WFEDWGQGTTLVTSVSAEGKSSGSGSESKPG-DVMTNPNPLSLPVSLGQDASISCRSSQSL 177  
 Db 122 TYDDWGQGTTLTVSSGGGGGGGGSDVMTQSPSLPVSLGQDASISCRSSQSLV 181  
 QY 178 HSNGITLHWYLOKPGSPKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGV 237  
 Db 182 HSNKGYTLHWYLOKPGSPKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGV 241  
 QY 238 YFCSQSTHVPYTFGGGKLEIKEEK 262  
 Db 242 YFCSQSTHVPYTFGGGKLEIKEEK 266  
 RESULT 10  
 AAM47634  
 ID AAM47634 standard; Protein; 271 AA.  
 XX AC AAM47634;  
 XX AC  
 XX DT 15-FEB-2002 (first entry)  
 XX DT  
 XX DE Murine MABL-2 #4.  
 XX XX  
 XX KW Murine; cytostatic; antiinflammatory; antianaemic; vasotropic;  
 KW antibody; signal transmission; cancer; inflammation; hormonal disorder;  
 KW leukaemia; lymphoma; aplastic anaemia; skeletal malformation.  
 XX  
 XX OS Mus sp.  
 XX XX  
 XX PN WO200179494-A1.  
 XX XX  
 XX PD 25-OCT-2001.  
 XX XX  
 XX PF 17-APR-2001; 2001WO-JP03288.  
 XX XX  
 XX PR 17-APR-2000; 2000JP-0115246.  
 XX PR 20-OCT-2000; 2000JP-0321821.  
 XX PR 20-OCT-2000; 2000JP-0321822.  
 XX PR 12-MAR-2001; 2001WO-JP01912.  
 XX XX  
 XX PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX XX  
 XX PI Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;  
 XX WPI; 2002-066368/09.  
 XX DR N-PSDB; ABA04525.  
 XX DR  
 XX XX Antibodies for treatment of diseases associated with cell  
 PT proliferation, hormonal disorders and cytokines comprise agonist  
 PT activity to signal transmission across cell membranes -  
 XX  
 XX PS Disclosure; Page 133-135; 173pp; Japanese.  
 XX PS  
 XX CC The present invention relates to modified antibodies. The antibodies  
 CC contain two or more H chain V domains and two or more L chain V domains  
 CC of a monoclonal antibody (MAB) which is capable of transmitting a signal  
 CC across the cell membrane by cross-linking a cell surface molecule, where  
 CC the antibodies can serve as signal transmission agonists. The antibodies  
 CC are useful for treatment and prevention of a broad range of disorders in  
 CC which signal transmission is implicated, such as cancer, inflammation, and  
 CC hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and  
 CC skeletal malformations. The present sequence was used to illustrate the

CC present invention.

XX Sequence 271 AA;

SQ

Query Match 70.3%; Score 978.5; DB 23; Length 271;

Best Local Similarity 74.0%; Pred. No. 3.2e-68; Indels 7; Gaps 3;

Matches 196; Conservative 19; Mismatches 43; Indels 7; Gaps 3;

3 SAIVLYVLLAAAHSAFAAVQLQOQSGAELVRPGASVTLSCKASGYTFTDYEIHVWRQTPV 62

4 SCILF--LVATATGVDSQVQLQOQSGPELVKPGASVKMSCKASGYTFANHVIHWKQKPG 61

63 HGLEWICAIIDPETGCTAYNOKFKDKAIVTDKSSSTAYMELRLSLTSDSAVYYTR---- 118

62 QGLEWIGYIYPYNDGTYKNEKPKDKATLTSDKSTTAYMDLSSLASDASVYYCARGGY 121

119 WFDWQCGTTLVTVAECKSGSGSEKPG--DVVMTNPISLPVSLGQASISCRSSQSL 177

122 TYDDWQCGTTLTVSSGG 181

178 HSGKITLHWYLOKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEAEDLGV 237

182 HSGKITLHWYLOKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEAEDLGV 241

238 YFCSQSTHVPYTFGGGTKLEIK 262

242 YFCSQSTHVPYTFGGGTKLEIKDYK 266

RESULT 11

AAG67499 standard; Protein; 533 AA.

AAG67499;

26-NOV-2001 (first entry)

Amino acid sequence of a murine antibody L chain.

XX Apoptosis; nucleated blood cell; integrin-associated protein; IAP;

XX erythrocyte agglutination; blood disease; leukemia; myeloma;

XX Hodgkin's disease; non-Hodgkin's lymphoma.

XX Mus sp.

WO200166737-A1.

13-SEP-2001.

12-MAR-2001; 2001WO-JP01912.

10-MAR-2000; 2000US-0523095.

17-APR-2000; 2000JP-0115246.

20-OCT-2000; 2000JP-0321822.

(CHUS ) CHUGAI SEIYAKU KK.

Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;

WPI; 2001-570772/64.

N-PSDB; AAH78156.

Reconstituted polypeptide induces apoptosis in nucleated blood cells

that contain integrin-associated protein (IAP), is useful for the

treatment of blood diseases such as leukemia -

Example 6; Page 123-126; 141pp; Japanese.

The specification describes a reconstituted polypeptide, which

induces apoptosis in nucleated blood cells that contain

integrin-associated protein (IAP). The polypeptide binds to IAP

without causing agglutination of erythrocytes. The polypeptide

contains at least two H chain V domains and at least two L chain

domains

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC V domains of a monoclonal antibody which induces apoptosis in

CC nuclear blood cells having IAP. The reconstituted polypeptide is used

CC for the treatment of blood diseases such as acute or chronic myeloid

CC leukemia, acute or chronic lymphoid leukemia, adult T-cell leukemia,

CC multiple myeloma, mixed leukemia, hairy cell leukemia, Hodgkin's

CC disease or non-Hodgkin's lymphoma. The present sequence represents a

CC murine monoclonal antibody L chain, which is used in the course of

CC the invention.

XX Sequence 533 AA;

SQ

Query Match 70.0%; Score 973.5; DB 22; Length 533;

Best Local Similarity 74.4%; Pred. No. 1.7e-67; Indels 7; Gaps 3;

Matches 195; Conservative 18; Mismatches 42; Indels 7; Gaps 3;

3 SAIVLYVLLAAAHSAFAAVQLQOQSGAELVRPGASVTLSCKASGYTFTDYEIHVWRQTPV 62

4 SCILF--LVATATGVDSQVQLQOQSGPELVKPGASVKMSCKASGYTFANHVIHWKQKPG 61

63 HGLEWICAIIDPETGCTAYNOKFKDKAIVTDKSSSTAYMELRLSLTSDSAVYYTR---- 118

62 QGLEWIGYIYPYNDGTYKNEKPKDKATLTSDKSTTAYMDLSSLASDASVYYCARGGY 121

119 WFDWQCGTTLVTVAECKSGSGSEKPG--DVVMTNPISLPVSLGQASISCRSSQSL 177

122 TYDDWQCGTTLTVSSGG 181

178 HSGKITLHWYLOKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEAEDLGV 237

182 HSGKITLHWYLOKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEAEDLGV 241

238 YFCSQSTHVPYTFGGGTKLEIK 259

242 YFCSQSTHVPYTFGGGTKLEIK 263

RESULT 12

ABG35317

ID ABG35317 standard; Protein; 533 AA.

XX

AC ABG35317;

XX

DT 30-JUL-2002 (first entry)

XX

DE Thrombopoietin agonist antibody associated protein #11.

XX Modified antibody; thrombopoietin; TPO; agonist;

XX TPO receptor; platelet reduction-associated blood disease;

XX thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.

XX Mus sp.

WO200233072-A1.

XX

PD 25-APR-2002.

XX

PF 22-OCT-2001; 2001WO-JP09259.

XX

PR 20-OCT-2000; 2000JP-0321821.

XX

PR 17-APR-2001; 2001WO-JP03288.

XX

PR 12-SEP-2001; 2001JP-0277314.

XX

PA (CHUS ) CHUGAI SEIYAKU KK.

XX

PI Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;

XX

DR WPI; 2002-383513/41.

XX

DR N-PSDB; ABK71335.

CC

XX

SQ

Query Match 70.3%; Score 978.5; DB 23; Length 271;

Best Local Similarity 74.0%; Pred. No. 3.2e-68; Indels 7; Gaps 3;

Matches 196; Conservative 19; Mismatches 43; Indels 7; Gaps 3;

3 SAIVLYVLLAAAHSAFAAVQLQOQSGAELVRPGASVTLSCKASGYTFTDYEIHVWRQTPV 62

4 SCILF--LVATATGVDSQVQLQOQSGPELVKPGASVKMSCKASGYTFANHVIHWKQKPG 61

63 HGLEWICAIIDPETGCTAYNOKFKDKAIVTDKSSSTAYMELRLSLTSDSAVYYTR---- 118

62 QGLEWIGYIYPYNDGTYKNEKPKDKATLTSDKSTTAYMDLSSLASDASVYYCARGGY 121

119 WFDWQCGTTLVTVAECKSGSGSEKPG--DVVMTNPISLPVSLGQASISCRSSQSL 177

122 TYDDWQCGTTLTVSSGG 181

178 HSGKITLHWYLOKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEAEDLGV 237

182 HSGKITLHWYLOKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEAEDLGV 241

238 YFCSQSTHVPYTFGGGTKLEIK 262

242 YFCSQSTHVPYTFGGGTKLEIKDYK 266

RESULT 11

AAG67499 standard; Protein; 533 AA.

AAG67499;

26-NOV-2001 (first entry)

Amino acid sequence of a murine antibody L chain.

XX Apoptosis; nucleated blood cell; integrin-associated protein; IAP;

XX erythrocyte agglutination; blood disease; leukemia; myeloma;

XX Hodgkin's disease; non-Hodgkin's lymphoma.

XX Mus sp.

WO200166737-A1.

13-SEP-2001.

12-MAR-2001; 2001WO-JP01912.

10-MAR-2000; 2000US-0523095.

17-APR-2000; 2000JP-0115246.

20-OCT-2000; 2000JP-0321822.

(CHUS ) CHUGAI SEIYAKU KK.

Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;

WPI; 2001-570772/64.

N-PSDB; AAH78156.

Reconstituted polypeptide induces apoptosis in nucleated blood cells

that contain integrin-associated protein (IAP), is useful for the

treatment of blood diseases such as leukemia -

Example 6; Page 123-126; 141pp; Japanese.

The specification describes a reconstituted polypeptide, which

induces apoptosis in nucleated blood cells that contain

integrin-associated protein (IAP). The polypeptide binds to IAP

without causing agglutination of erythrocytes. The polypeptide

contains at least two H chain V domains and at least two L chain

domains

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC



N-PSDB; ABA04532.

Antibodies for treatment of diseases associated with cell proliferation, hormonal disorders and cytokines comprise activity to signal transmission across cell membranes - Disclosure; Page 141-145; 173pp; Japanese.

The present invention relates to modified antibodies. The antibodies contain two or more H chain V domains and two or more L chain V domains of a monoclonal antibody (Mab) which is capable of transmitting a signal across the cell membrane by cross-linking a cell surface molecule, where the antibodies can serve as signal transduction agonists. The antibodies are useful for treatment and prevention of a broad range of disorders in which signal transduction is implicated, such as cancer, inflammation, CC hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and skeletal malformations. The present sequence was used to illustrate the present invention.

Query Match 70.0%; Score 973.5; DB 23; Length 533;  
Best Local Similarity 74.4%; Pred No. 1.7e-67;  
Matches 195; Conservative 18; Mismatches 42; Indels 7; Gaps

QY 3 SAIVLYLVLLAAAHSAFAAVOLQQSGAELVRPGASVTLSCKASGYTFTDYIEIHWVROTPV 62  
Dd :|::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 4 SCIIILF--LVAATGVDSDQVLQQSGPELVKPCASVKMSCKASGYTFANHVIHWWKKP 61  
QY 63 HGLEWIGAIIDPETGTAYNOKFKDKAIVTVDKSSSTAYMEIRLSLTSEDSAVYYTYR---- 118  
Dd |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 62 QGLEWIGIYIPNDGTKYNEKFDDKATLTSDKSSTAYMDLSLASSEDASVYYCARGGY 121  
QY 119 WFDWMQGCTLTVTASAEGSKSGSESKEGP-DVMVMTNPPLSLPVSLGLDOAISICRSQSULL 177  
Dd |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 122 TYDDMQGGTTITVSSGGCGGGGGGVDMVPDPFRFGSGSVTDFTLMISRVEADLG 181  
QY 178 HSNGITYLHWYLOKPQSPKLIIYKVNSRFSGVPDRFPFGSGGSQTDTLKISRVAEADLG 237  
Dd |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 182 HSNKITLHLWLQPKQPSPKLIIYKVNSRFSGVPDRFPFGSGSVTDFTLMISRVEADLG 241  
QY 238 YFCSQSTHVPTFFGGTKLEIK 259  
Dd |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 242 YFCSQSTHVPTFFGGTKLEIK 263

RESULT 14  
AAB23817 standard; Protein; 274 AA.  
AC AAB23817;  
XX Murine MabL-2 #6.  
XX Murine; cytostatic; antiinflammatory; antianaemic; vasotropic;  
DX antibody; signal transduction; cancer; inflammation; hormonal disorder;  
TX leukaemia; lymphoma; aplastic anaemia; skeletal malformation.  
DE Mus sp.  
KW WO200179494-A1.  
XW 25-OCT-2001.  
OS 17-APR-2001; 2001WO-JP03288.  
PN 17-APR-2000; 2000JP-0115246.  
XX R 20-OCT-2000; 2000JP-0321821.  
PD 20-OCT-2000; 2000JP-0321822.  
PF 12-MAR-2001; 2001WO-JP01912.  
PP (CHUS ) CHUGAI SEIYAKU KK.  
PR Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;  
PA WPI; 2002-066368/09.  
PX WPI; 2002-066368/09.  
PI D.



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

IQM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 18:44:54 ; Search time 1122 Seconds  
(without alignments)  
11980.619 Million cell updates/sec

Title: US-09-358-321C-31

Perfect score: 830  
Sequence: 1 tctgaatggttaagcgctat.....ctgaattagtaagcgccgc 830

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthm:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rnd:\*

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	317.6	38.3	926	14	BQ959057
2	316	38.1	678	13	BQ962941
3	316	38.1	925	13	BQ963141
4	314.4	37.9	997	13	B1107100
5	312.2	37.6	962	12	BF578262
6	309.2	37.3	793	10	BE307894

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	308	37.1	693	13	BQ964281
8	302.2	36.4	716	13	BQ964192
9	300.2	36.2	743	13	BQ968770
10	296.6	35.7	965	12	BF577927
11	293.6	35.4	913	14	BQ933319
12	280.8	33.8	509	17	A2791472
13	279.6	33.7	898	12	BF135785
14	278.2	33.5	755	13	B1109046
15	277.8	33.5	884	13	BQ963735
16	276.6	33.3	772	10	BE285427
17	276.4	33.3	707	13	B1250555
18	262.2	31.6	1018	14	BQ934943
19	247	29.8	766	13	BQ969524
20	240.6	29.0	512	12	BF023434
21	240	28.9	723	13	BQ969577
22	240	28.9	952	12	BQ758592
23	236.6	28.5	995	14	BQ712430
24	236.4	28.5	1576	11	AK007918
25	235.2	28.3	898	14	BQ708918
26	235.2	28.3	960	14	BQ711007
27	234.8	28.3	640	14	BQ109114
28	233.6	28.1	471	10	AW405772
29	232	28.0	614	10	AW405187
30	230.2	27.7	634	14	BM783161
31	228.6	27.5	454	10	AW408883
32	228	27.5	909	13	B1105366
33	227.2	27.4	896	13	BQ963760
34	227	27.3	967	13	BQ964352
35	226	27.2	491	12	BF174573
36	225.4	27.2	522	13	BM511309
37	225.4	27.2	751	12	BQ542438
38	224.4	27.0	598	13	B1104341
39	224.4	27.0	829	12	BF144014
40	224	27.0	696	13	B1838136
41	223.8	27.0	363	9	AA464313
42	223.8	27.0	488	10	AW405725
43	223.8	27.0	990	13	B1838327
44	223.6	26.9	739	10	BE284158
45	223.4	26.9	488	14	H25625

## ALIGNMENTS

RESULT 1

BQ959057

LOCUS

DEFINITION

AGENCOURT\_10049748 NCI CGAP Co24 Mus musculus cDNA clone

IMAGE:6479377 5', mRNA sequence.

ACCESSION

BQ959057

VERSION

BQ959057.1 GI:22374535

KEYWORDS

EST.

SOURCE

house mouse

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

NIH-MGC http://mgc.nci.nih.gov/.

Tissue Procurement: The Cepko Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Unpublished (1999)

Contract: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14024 row: h column: 02

High quality sequence stop: 692.

Location/Qualifiers

1..926

BQ959057 926 bp mRNA linear EST 21-AUG-2002

AGENCOURT\_10049748 NCI CGAP Co24 Mus musculus cDNA clone

IMAGE:6479377 5', mRNA sequence.

ACCESSION

BQ959057

VERSION

BQ959057.1 GI:22374535

KEYWORDS

EST.

SOURCE

house mouse

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

NIH-MGC http://mgc.nci.nih.gov/.

Tissue Procurement: The Cepko Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Unpublished (1999)

Contract: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14024 row: h column: 02

High quality sequence stop: 692.

Location/Qualifiers

1..926

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6479377"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 237 a 251 c 202 g 235 t 1 others
ORIGIN
Query Match 38.3%; Score 317.6; DB 14; Length 926;
Best Local Similarity 95.9%; Pred. No. 7 le-85;
Matches 326; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 444 CCGGGATGTTGATGACCCCAACCCACTCTCCCTGCTGTCAGTCTTGGAGATCAAGC 503
Db 86 CAGTGATGTTGATGACCCCAACCCACTCTCCCTGCTGTCAGTCTTGGAGATCAAGC 145
QY 504 CTCCTATCTTGCAGATCTAGTCAGAGCCCTTTTACACAGTAAATGGAATCACCTATTACA 563
Db 146 CTCCTATCTTGCAGATCTAGTCAGAGCCCTTTTACACAAATAATGGAACACCTATTACA 205
QY 564 TTGGTACCTGACAGCCAGCCAGCTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCG 623
Db 206 TTGGTACCTGACAGCCAGCCAGCTCTCCAAAGCTCTGATCTACAAAGTTTCTAACCG 265
QY 624 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAA 683
Db 266 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAA 325
QY 684 GATCAGAGATGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
Db 326 GATCAGAGATGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATAT 385
QY 744 TCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATAAAAA 783
Db 386 TCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATAAAAA 425

RESULT 2
LOCUS BG962941 678 bp mRNA linear EST 12-JUN-2001
DEFINITION 60282725F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982670 5', mRNA sequence.
ACCESSION BG962941
VERSION BG962941.1 GI:14350578
KEYWORDS EST.
SOURCE house mouse, Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 678) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS Unpublished (1999)
TITLE Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgapbs@mail.nih.gov
COMMENT Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10986 row: a column: 07
High quality sequence stop: 676.
Location/Qualifiers 1..678
FEATURES source
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6479377"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 237 a 251 c 202 g 235 t 1 others
ORIGIN
Query Match 38.3%; Score 317.6; DB 14; Length 926;
Best Local Similarity 95.9%; Pred. No. 7 le-85;
Matches 326; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 444 CCGGGATGTTGATGACCCCAACCCACTCTCCCTGCTGTCAGTCTTGGAGATCAAGC 503
Db 86 CAGTGATGTTGATGACCCCAACCCACTCTCCCTGCTGTCAGTCTTGGAGATCAAGC 145
QY 504 CTCCTATCTTGCAGATCTAGTCAGAGCCCTTTTACACAGTAAATGGAATCACCTATTACA 563
Db 146 CTCCTATCTTGCAGATCTAGTCAGAGCCCTTTTACACAAATAATGGAACACCTATTACA 205
QY 564 TTGGTACCTGACAGCCAGCCAGCTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCG 623
Db 206 TTGGTACCTGACAGCCAGCCAGCTCTCCAAAGCTCTGATCTACAAAGTTTCTAACCG 265
QY 624 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAA 683
Db 266 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAA 325
QY 684 GATCAGAGATGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
Db 326 GATCAGAGATGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATAT 385
QY 744 TCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATAAAAA 783
Db 386 TCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATAAAAA 425

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/clone="IMAGE:4982670"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 181 a 173 c 158 g 166 t
ORIGIN
Query Match 38.1%; Score 316; DB 13; Length 678;
Best Local Similarity 95.6%; Pred. No. 2e-84;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 444 CCGGGATGTTGATGACCCCAACCCACTCTCCCTGCTGTCAGTCTTGGAGATCAAGC 503
Db 74 CAGTGATGTTGATGACCCCAACCCACTCTCCCTGCTGTCAGTCTTGGAGATCAAGC 133
QY 504 CTCCTATCTTGCAGATCTAGTCAGAGCCCTTTTACACAGTAAATGGAATCACCTATTACA 563
Db 134 CTCCTATCTTGCAGATCTAGTCAGAGCCCTTTTACACAGTAAATGGAACACCTATTACA 193
QY 564 TTGGTACCTGACAGCCAGCCAGCTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCG 623
Db 194 TTGGTACCTGACAGCCAGCCAGCTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCG 253
QY 624 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAA 683
Db 254 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAA 313
QY 684 GATCAGAGATGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
Db 314 GATCAGAGATGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 373
QY 744 TCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATAAAAA 783
Db 374 TCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATAAAAA 413

RESULT 3
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DEFINITION 602828165F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982705 5', mRNA sequence.
ACCESSION BG963141
VERSION BG963141.1 GI:14350778
KEYWORDS EST.
SOURCE house mouse, Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 925) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS Unpublished (1999)
TITLE Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgapbs@mail.nih.gov
COMMENT Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10986 row: b column: 18
High quality sequence stop: 729.
Location/Qualifiers 1..925
FEATURES source
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4982705"

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/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (fl-phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

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BASE COUNT      245 a      246 c      206 g      228 t
ORIGIN

Query Match      38.1%; Score 316; DB 13; Length 925;
Best Local Similarity 95.6%; Pred. No. 2.2e-84;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 444 CGGGGATGTTGTGATGACCCCAACCCACTCTCCCTGCCCTGTCAGTTTGGAGATCAAGC 503
DB 75 CAGTGATGTTGTGATGACCCCAACCCACTCTCCCTGCCCTGTCAGTTTGGAGATCAAGC 134
QY 504 CTCCATCTCTTGAGATCTAGTCAGAGCCITTTACACAGTAATGGAATCACTATTATACA 563
DB 135 CTCCATCTCTTGAGATCTAGTCAGAGCCITTTACACAGTAATGGAATCACTATTATACA 194
QY 564 TTGTTACTCTGAGAAGCCAGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAACCG 623
DB 195 TTGTTACTCTGAGAAGCCAGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAACCG 254
QY 624 ATTTCTGGGGTCCACACAGGTTTCAGTGGCAGTGGATCAGGACACATTTCACTCAA 683
DB 255 ATTTCTGGGGTCCACACAGGTTTCAGTGGCAGTGGATCAGGACACATTTCACTCAA 314
QY 684 GATCAGCAGAGTGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
DB 315 GATCAGCAGAGTGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 374
QY 744 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAAA 783
DB 375 TCCATTACGTTCCGTCGGGACAAAGTTTGGAAATAAAAA 414

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RESULT 4
BI107100
LOCUS      602894523F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5039788 5',
DEFINITION mRNA sequence.
ACCESSION BI107100
VERSION    BI107100.1 GI:14557993
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 997)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1109 row: m column: 05
High quality sequence stop: 832.
Location/Qualifiers
1..997
/organism="Mus musculus"
/strain="CZECH II"
/db xref="taxon:10090"
/clone="IMAGE:5039788"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."

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FEATURES
source

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Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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BASE COUNT      270 a      272 c      213 g      242 t
ORIGIN

Query Match      37.9%; Score 314.4; DB 13; Length 997;
Best Local Similarity 95.3%; Pred. No. 6.8e-84;
Matches 324; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 444 CGGGGATGTTGTGATGACCCCAACCCACTCTCCCTGCCCTGTCAGTTTGGAGATCAAGC 503
DB 83 CAGTGATGTTTGTGATGACCCCAACCCACTCTCCCTGCCCTGTCAGTTTGGAGATCAAGC 142
QY 504 CTCCATCTCTTGAGATCTAGTCAGAGCCITTTACACAGTAATGGAATCACTATTATACA 563
DB 143 CTCCATCTCTTGAGATCTAGTCAGAGCCITTTACACAGTAATGGAATCACTATTATACA 202
QY 564 TTGTTACTCTGAGAAGCCAGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAACCG 623
DB 203 TTGTTACTCTGAGAAGCCAGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAACCG 262
QY 624 ATTTCTGGGGTCCACACAGGTTTCAGTGGCAGTGGATCAGGACACATTTCACTCAA 683
DB 263 ATTTCTGGGGTCCACACAGGTTTCAGTGGCAGTGGATCAGGACACATTTCACTCAA 322
QY 684 GATCAGCAGAGTGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
DB 323 GATCAGCAGAGTGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 382
QY 744 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAAA 783
DB 383 TCCGTATACGTTCCGATCGGGGACCAAGCTGGAATAAAAA 422

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RESULT 5
BF578262
LOCUS      602093093F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4207582 5',
DEFINITION mRNA sequence.
ACCESSION BF578262
VERSION    BF578262.1 GI:11651974
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 962)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9770 row: i column: 23
High quality sequence stop: 681.
Location/Qualifiers
1..962
/organism="Mus musculus"
/strain="FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:4207582"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (fl-phage-resistant)"

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FEATURES
source

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/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 262 a 253 c 221 g 226 t  
ORIGIN

Query Match 37.6%; Score 312.2; DB 12; Length 962;  
Best Local Similarity 94.7%; Pred. No. 3.1e-83;  
Matches 323; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 443 CCGGGGATGTGTGATGACCCCAACCACTCTCCCTGCTGTGAGTCTGGAGATCAAG 502  
DB 85 CCAAGTGTGTGTGATGACCCCAACCACTCTCCCTGCTGTGAGTCTGGAGATCAAG 144  
QY 503 CTTCCATCTCTTGCAGATCTAGTCAGAGCCCTTTTACACAGTCAATGGAATCACTATTATAC 562  
DB 145 CTTCCATCTCTTGCAGATCTAGTCAGAGCCCTTTTACACAGTCAATGGAATCACTATTATAC 204  
QY 563 ATTGGTACCTGCAGAACCCAGGCCAGTCTCCAAAGCTCTCGATCTACAAAGTTTCCAAAC 622  
DB 205 ATTGGTACCTGCAGAACCCAGGCCAGTCTCCAAAGCTCTCGATCTCGCAAACTTTCCAACC 264  
QY 623 GATTTCTGGGGTCCAGACAGAGTTTCAAGTGCAGTGCAGGACAGATTTACACTCA 682  
DB 265 GATTTCTGGGGTCCAGACAGAGTTTCAAGTGCAGTGCAGGACAGATTTACACTCA 324  
QY 683 AGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACACATG 742  
DB 325 AGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACACATA 384  
QY 743 TTCGTTACAGTTTCGGAGGGGGACCAAGCTGGAAATAAAA 783  
DB 385 TTCCATTACAGTTTCGGCTCGGGGACCAAGTTGGAAATAAAA 425

RESULT 6  
BE307894 793 bp mRNA linear EST 26-OCT-2000  
LOCUS 601096548F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3491195 5',  
DEFINITION mRNA sequence.  
ACCESSION BE307894  
VERSION BE307894.1 GI:9163704  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 793)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM8534 row: p column: 12  
High quality sequence stop: 514.  
Location/Qualifiers  
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/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3491195"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"

FEATURES  
source

1. .793  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3491195"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 156 a 210 c 217 g 210 t  
ORIGIN

Query Match 37.3%; Score 309.2; DB 10; Length 793;  
Best Local Similarity 94.7%; Pred. No. 2.4e-82;  
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 446 GGGATGTTGTGATGACCCCAACCACTCTCCCTGCTGTGAGTCTGGAGATCAAGCCT 505  
DB 80 GTGATGTTGTGATGACCCCAACCACTCTCCCTGCTGTGAGTCTGGAGATCAAGCCT 139  
QY 506 CCATCTCTTGCAGATCTAGTCAGAGCCCTTTTACACAGTCAATGGAATCACTATTATACAT 565  
DB 140 CCATCTCTTGTAGATCTAGTCAGAGCCCTTTTACACAGTCAATGGAATCACTATTATACAT 199  
QY 566 GGTACCTGCAGAACCCAGGCCAGTCTCCAAAGCTCTCGATCTACAAAGTTTCCAAACCGAT 625  
DB 200 GGTCTCTGCAGAACCCAGGCCAGTCTCCAAAGCTCTCGATCTACAAAGTTTCCAAACCGAT 259  
QY 626 TTTCTGGGTCCAGACAGGTTTCAAGTGCAGTGGATGAGGACAGATTTTCACTCAAGA 685  
DB 260 TTTCTGGGTCCAGACAGGTTTCAAGTGCAGTGGATGAGGACAGATTTTCACTCAAGA 319  
QY 686 TCAGCAGATGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACACATGTTTC 745  
DB 320 TCACCAGATGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACACATGTTTC 379  
QY 746 CGTACACGTTTCGGAGGGGGACCAAGCTGCAATAAAA 783  
DB 380 CGCTACGTTTCGGTCTGGGACCAAGCTGGAGCTGAAA 417

RESULT 7  
BG964281 693 bp mRNA linear EST 12-JUN-2001  
LOCUS 602829076F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4983618 5',  
DEFINITION mRNA sequence.  
ACCESSION BG964281  
VERSION BG964281.1 GI:14351918  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 693)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10988 row: h column: 19  
High quality sequence stop: 553.  
Location/Qualifiers  
1. .693  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4983618"  
/clone\_lib="NCI\_CGAP\_Co24"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;

FEATURES  
source

1. .693  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4983618"  
/clone\_lib="NCI\_CGAP\_Co24"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: Sali; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 179 a 184 c 160 g 169 t

ORIGIN

Query Match 37.1%; Score 308; DB 13; Length 693;

Best Local Similarity 94.1%; Pred. No. 5.4e-82;

Matches 320; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 444 CGGGGATGTTCTGATGACCCCAACCACTCTCCCTGCTGTGAGTCTTGAGATCAAGC 503

DB 89 CAGTGATGTTGTTGACCCAACTCCACTCTCCCTGCTGTGAGTCTTGAGATCAAGC 148

QY 504 CTCATCTCTTTCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACTATTAC 563

DB 149 CTCATCTCTTTCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACTATTAC 208

QY 564 TTGTACTCTGAGAACCCAGCCAGTCTCCAAAGCTCTGATCTACAAGTTTCCAACCG 623

DB 209 TTGTACTCTGAGAACCCAGCCAGTCTCCAAAGCTCTGATCTACAAGTTTCCAACCG 268

QY 624 ATTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAA 683

DB 269 ATTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAA 328

QY 684 GATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 743

DB 329 GATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAATACACATGT 388

QY 744 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAA 783

DB 389 TCCGTGACGTTCCGTGGAGGCCACCAAACTGGAATAAAA 428

RESULT 8

LOCUS BG964192 716 bp mRNA linear EST 12-JUN-2001

DEFINITION 602828968F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4983617 5',

mRNA sequence.

ACCESSION BG964192

VERSION BG964192.1 GI:14351829

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM10988 row: h column: 18

High quality sequence stop: 716.

Location/Qualifiers

1. 716

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:4983617"

/lab\_host="NCI CGAP Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;

Site 2: Sali; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 199 a 196 c 181 g 167 t

Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 191 a 188 c 163 g 174 t

ORIGIN

Query Match 36.4%; Score 302.2; DB 13; Length 716;

Best Local Similarity 94.6%; Pred. No. 3.1e-80;

Matches 313; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 453 TGTGATGACCCCAACCACTCTCCCTGCTGTGAGTCTTGAGATCAAGCTTCATCTC 512

DB 97 TGTGTTGACCCCAACCACTCTCCCTGCTGTGAGTCTTGAGATCAAGCTTCATCTC 156

QY 513 TTCCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACTATTACATTTGTTACCT 572

DB 157 TTCCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACTATTACATTTGTTACCT 216

QY 573 GCAGAGCCAGGCGCAGTCTCCAAAGCTCTGATCTCAAAAGTTTCCAACCGATTCTGG 632

DB 217 GCAGAGCCAGGCGCAGTCTCCAAAGCTCTGATCTCAAAAGTTTCCAACCGATTCTGG 276

QY 633 GGTCCACAGACAGTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAAGATCAGCAG 692

DB 277 GGTCCACAGACAGTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAAGATCAGCAG 336

QY 693 AGTGGAGGCTGAGATCTGGGAGTTTATTTCTGCTCAAAAGTACACATGTTCCGTACAC 752

DB 337 AGTGGAGGCTGAGATCTGGGAGTTTATTTCTGCTCAAAAGTACACATGTTCCGTACAC 396

QY 753 GTTCGGAGGGGGACCAAGCTGGAATAAAA 783

DB 397 GTTCGGAGGGGGACCAAGCTGGAATAAAA 427

RESULT 9

LOCUS BG968770

DEFINITION 602836677F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4990962 5',

mRNA sequence.

ACCESSION BG968770

VERSION BG968770.1 GI:14356407

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 743)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM11007 row: j column: 19

High quality sequence stop: 659.

Location/Qualifiers

1. 743

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:4990962"

/lab\_host="NCI CGAP Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;

Site 2: Sali; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 199 a 196 c 181 g 167 t

## ORIGIN

Query Match 36.2%; Score 300.2; DB 13; Length 743;  
 Best Local Similarity 94.4%; Pred. No. 1.3e-79;  
 Matches 322; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 444 CGGGGATGTTGTGATGACCCCAACCCCACTCTCCCTGCCCTGTGAGTCTTGGAGATCAAGC 503  
 DB 68 CAGTGATGTTGTGATGACCCCAACCTCCACTCTCCCTGCCCTGTGAGTCTTGGAGATCAAGC 127  
 QY 504 CTCATCTCTTGAGATCTAGTCAGAGCCCTTTTACACAGTAATGGAATCACTATTATACA 563  
 DB 128 CTCATCTCTTGAGATCTAGTCAGAGCCCTTTTACACAGTAATGGAATCACTATTATACA 187  
 QY 564 TTGTGTACTCTGAGAACCCAGCCAGTCTCCAAAGCTCCTGATCTTACAAAGTTTCCAAACCG 623  
 DB 188 TTGTGTACTCTGAGAACCCAGCCAGTCTCCAAAGCTCCTGATCTTACAAAGTTTCCAAACCG 247  
 QY 624 ATTTCTGGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAA 683  
 DB 248 ATTTCTGGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAA 307  
 QY 684 GATCA-CCAGAGTGGAGCTGAGGATCTGGAGTTTATTCTGCTCTCAAAGTACACATG 742  
 DB 308 GATCACGTAGTGGAGCTGAGGATCTGGAGTTTATTCTGCTCTCAAAGTACACATG 367  
 QY 743 TTCGTCACGTTTCGGAGGGGGACCAAGCTGGAATAAAAA 783  
 DB 368 TTCGCTCACGTTTCGGTGTGGGACCAAGCTGGAGCTGGAATAAAAA 408

RESULT 10  
 BF577927  
 LOCUS 602091947F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4206515 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF577927  
 VERSION BF577927  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 965)  
 NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LAM9767 row: m column: 12  
 High quality sequence stop: 665.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4206515"  
 /clone\_lib="NCI\_CGAP\_Co24"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.6 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT  
 ORIGIN

269 a 241 c 242 g 213 t

Query Match 35.7%; Score 296.6; DB 12; Length 965;  
 Best Local Similarity 95.5%; Pred. No. 1.7e-78;  
 Matches 316; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 453 TGTGATGACCCCAACCCCACTCTCCCTGCCCTGTGAGTCTTGGAGATCAAGCTTCATCTC 512  
 DB 92 TGTGATGACCCCAACCTCCACTCTCCCTGCCCTGTGAGTCTTGGAGATCAAGCTTCATCTC 151  
 QY 513 TTGCAGATCTAGTCAGAGCCCTTTTACACAGTAATGGAATCACTATTATACATTGGTACCT 572  
 DB 152 TTGCAGATCTAGTCAGAGCCCTGGTACACAGTAATGGAATCACTATTATACA-TGGTACCT 210  
 QY 573 GCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTTACAAAGTTTCCAAACCGATTTCCTGG 632  
 DB 211 GCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTTACAAAGTTTCCAAACCGATTTCCTGG 270  
 QY 633 GGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAAGATCAGCAG 692  
 DB 271 GGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAAGATCAGCAG 330  
 QY 693 AGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAAGTACACATGTTCCCGTACAC 752  
 DB 331 AGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAAGTACACATGTTCCCGTACAC 390  
 QY 753 GTTCGGAGGGGGACCAAGCTGGAATAAAAA 783  
 DB 391 GTTCGGTGGAGGCCACCAAGCTGGAATAAAAA 421

RESULT 11  
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 LOCUS AGENCOURT 8881916 NCI\_CGAP\_Co24 Mus musculus cDNA clone  
 DEFINITION IMAGE:6476417 5', mRNA sequence.  
 ACCESSION BQ933319  
 VERSION BQ933319  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 913)  
 NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LAM14016 row: 1 column: 18  
 High quality sequence start: 3  
 High quality sequence stop: 525.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6476417"  
 /clone\_lib="NCI\_CGAP\_Co24"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.6 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

FEATURES  
 source

1..913

Query Match

35.4%; Score 293.6; DB 14; Length 913;



Best Local Similarity 91.5%; Pred. No. 1.3e-77;  
Matches 311; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 444 CGGGATGTTGTGATGACCCCAACCCACTCTCCCTGCTGTGCTGTGAGATCAAGC 503  
Db 105 CAGTGATGTTGTGATGACCCCAACCCACTCTCCCTGCTGTGCTGTGAGATCAAGC 164  
QY 504 CTCATCTCTTGCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACTATTACA 563  
Db 165 CTCATCTCTTGCAGATCTAGTCAGAGTATGTACATAGTAATGGAATACCTTTTACA 224  
QY 564 TTGGTACTGTCAGAACCCAGGCGAGCTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACG 623  
Db 225 ATGGTACCTGCAGAAACCCAGGCGAGCTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACG 284  
QY 624 ATTTTCTGGGCTCCAGACAGGTTTCAGTGGCAGTGATCAGGACAGATTTTCACTCAA 683  
Db 285 ATTTTCTGGGCTCCAGACAGGTTTCAGTGGCAGTGATCAGGACAGATTTTCACTCAA 344  
QY 684 GATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACACATGT 743  
Db 345 GATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACACATGT 404  
QY 744 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAA 783  
Db 405 TCCGTGGAGCTTCGGTGGAGGACCAAGCTGGAATCAA 444

RESULT 12  
A2791472/c  
LOCUS A2791472 509 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0041H23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0041H23 F, DNA sequence.  
ACCESSION A2791472  
VERSION A2791472.1 GI:12934393  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 509)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0041 row: H column: 23  
Seq primer: CGTGTAAACAGCAGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 509.  
Location/Qualifiers  
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/organism="Mus musculus"  
/strain="C57BL/6J"  
/db xref="taxon:10090"  
/clone="UUGC2M0041H23"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (G14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 124 a 127 c 128 g 130 t  
ORIGIN

Query Match 33.8%; Score 280.8; DB 17; Length 509;  
Best Local Similarity 97.8%; Pred. No. 8.7e-74;  
Matches 285; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 69 GGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGGAGCCTGGGGCTTCAGTGACGCTGTC 128  
Db 327 GGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGGAGCCTGGGGCTTCAGTGACGCTGTC 268  
QY 129 CTGCAAGGCTTCGGGGCTACACATTTACTGACTATGAATACACTGGGTGAGGCAGACACC 188  
Db 267 CTGCAAGGCTTCGGGGCTACACATTTACTGACTATGAATACACTGGGTGAGGCAGACACC 208  
QY 189 TGTGCATGGCTGGAATGGATTTGGAGCTATTGATCTCGAAACTGGTGGTACTGCCTCAA 248  
Db 207 TGTGCATGGCTGGAATGGATTTGGAGCTATTGATCTCGAAACTGGTGGTACTGCCTCAA 148  
QY 249 TCAGAAGTTCAAGGACAAGCCATAGTACTGTAGACAAATCTCCAGCAGACGCTACAT 308  
Db 147 TCAGAAGTTCAAGGACAAGCCATAGTACTGTAGACAAATCTCCAGCAGACGCTACAT 88  
QY 309 GGAGCTCCGAGCCTGACATCTGAAAGACTCTGCGGCTATTACTATATACAAGA 360  
Db 87 GGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGCTATTACTGTACAAGA 36

RESULT 13  
BF135785  
LOCUS 601782072F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4010344 5',  
DEFINITION mRNA sequence.  
ACCESSION BF135785  
VERSION BF135785.1 GI:10974825  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 898)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9247 row: 0 column: 17  
High quality sequence stop: 4  
High quality sequence start: 520.  
Location/Qualifiers

FEATURES  
source

source		1. .898 /organism="Mus musculus" /strain="CZECH II" /db_xref="taxon:10090" /clone="IMAGE:4010344" /clone_lib="NCI_CGAP_Lu30" /tissue_type="tumor, metastatic to mammary" /lab_host="DH108" /notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies, NIH" Investigator providing samples: Gilbert Smith, NIH"		
BASE COUNT	222 a	237 c	215 g	224 t
ORIGIN				
	Query Match	33.7%;	Score 279.6;	DB 12; Length 898;
	Best Local Similarity	92.4%;	Pred No. 2.3e-73;	
	Matches 316;	Conservative	0;	Mismatches 24; Indels 2; Gaps 2;
QY	444	CGGGGATGTTGTGATGACCCCAAAACCCTTCCTCCCTGCCTGCTAGTCTTGAGATCAAGC	503	
Db	64	CAGTGATGTTGTGATGACCCCAAACCTCCACTTCCTCCCTGCTGAGTCTTGAGATCAAGC	123	
QY	504	CTCATCTCTTTGAGATCTTAGTCAGAGCCTTTTACACAGTAATGAATCACCTATT-TT-AC	562	
Db	124	CTCCATCTCTTTGAGATCTTAGTCAGAGCATTGTACACAGTAATGGAACACCTATT-TTAAT	183	
QY	563	ATTGGTACCTGCAGACGCCAGGCCAGTCTCCAAGCTCTCATCAAAAGTTTCCAACC	622	
Db	184	ATTGGTACCTGCAGAACCCAGGCCAGTCTCCAAGCTCTCATCAAAAGTTTCCAACC	243	
QY	623	GATTTTCTGGGGTCCCAGA-CAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACACTC	681	
Db	244	GATTTTCTGGGGTCCCAGACACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACACTC	303	
QY	682	AAGATCAGCAGATGGAGGCTGAGGATCTGGAGTTTATTTCCTCTCTAAAGTACACAT	741	
Db	304	AAGATCAGCAGATGGAGGCTGAGGATGAGGATGAGGATTTATTACTGCTTTCAAGGTACACAT	363	
QY	742	GTTCCTGACAGTTCGGAGGGGGGACCAAGCTGGATAAAA	783	
Db	364	GTTCCTGAGAGTTCGGTGGAGGCCAAGCTGGATAAAA	405	
RESULT 14				
B1109046		755 bp	mRNA	linear EST 26-JUN-2001
LOCUS	602896879F1 NCI_CGAP_Mam5 Mus musculus	cDNA clone IMAGE:5026770 5'		
DEFINITION	mRNA sequence.			
ACCESSION	B1109046			
VERSION	B1109046.1	GI:14559947		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	1 (bases 1 to 755)			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.			
COMMENT	Unpublished (1999) National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM11075 row: n column: 19 High quality sequence stop: 741. Location/Qualifiers			
FEATURES				

Search completed: May 17, 2003, 03:33:20  
Job time : 1138 secs

GenCore version 5.1.4 p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2003, 04:47:29 ; Search time 106 Seconds  
(without alignments)  
10100.459 Million cell updates/sec

Title: US-09-358-321C-31

Perfect score: 830  
Sequence: 1 tctgaatgtaagcgctat.....ctgaattagtaagcgcgcc 830

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 810007 seqs, 644969091 residues

Total number of hits satisfying chosen parameters: 1620014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510.8	61.5	879	10	US-09-978-752-22
2	419.4	50.5	1135	9	US-09-203-958-2
3	407.6	49.1	749	9	US-09-968-851-46
4	405.2	48.8	1611	9	US-09-968-851-37
5	361	43.5	723	10	US-09-978-752-7
6	351.4	42.3	4681	10	US-09-897-006-10
7	334	40.2	729	10	US-09-924-099-20
8	333.2	40.1	711	10	US-09-924-099-19
9	321	38.7	2090	9	US-10-060-585-6
10	320.4	38.6	384	10	US-09-753-436-44
11	320	38.6	336	9	US-09-518-737-3
12	319.4	38.5	1518	9	US-10-060-585-5
13	317.8	38.3	1807	9	US-10-060-585-2
14	316.4	38.1	1467	9	US-10-060-585-3
15	315.4	38.0	729	9	US-10-060-585-1
16	313.6	37.8	856	10	US-09-883-758-3
17	313.6	37.8	856	10	US-09-883-758-6
18	313.4	37.8	759	10	US-09-978-752-10
19	304.8	36.7	504	12	US-10-006-773-14

20	304.8	36.7	780	9	US-10-247-488-3	Sequence 3, Appli
21	304.2	36.7	771	9	US-10-247-488-1	Sequence 1, Appli
22	304	36.6	899	10	US-09-883-758-1	Sequence 1, Appli
23	304	36.6	899	10	US-09-883-758-5	Sequence 5, Appli
24	302.4	36.4	375	10	US-09-753-436-65	Sequence 65, Appli
25	301.6	36.3	729	9	US-09-726-258-41	Sequence 41, Appli
26	300.8	36.2	391	9	US-09-726-258-34	Sequence 34, Appli
27	300.4	36.2	10511	9	US-10-059-261-109	Sequence 109, App
28	299.8	36.1	717	10	US-10-162-889-5	Sequence 5, Appli
29	299.8	36.1	717	10	US-09-808-037-5	Sequence 6, Appli
30	297.6	35.9	339	10	US-09-978-752-6	Sequence 6, Appli
31	296.2	35.7	1143	10	US-09-822-698A-6	Sequence 6, Appli
32	295.2	35.6	447	10	US-09-990-205-1	Sequence 1, Appli
33	294.4	35.5	717	8	US-08-940-544-3	Sequence 3, Appli
34	290.8	35.0	920	10	US-09-742-693-28	Sequence 28, Appli
35	290.2	35.0	816	10	US-09-766-543-9	Sequence 9, Appli
36	288.4	34.7	720	10	US-09-976-787-30	Sequence 30, Appli
37	287	34.6	420	9	US-09-141-894-3	Sequence 3, Appli
38	286.6	34.5	717	9	US-10-151-882-11	Sequence 11, Appli
39	285.4	34.4	336	9	US-09-982-992A-3	Sequence 3, Appli
40	285.2	34.4	714	10	US-09-976-787-31	Sequence 31, Appli
41	285.2	34.4	779	9	US-09-887-853-3	Sequence 3, Appli
42	282.6	34.0	780	9	US-09-782-672-1	Sequence 1, Appli
43	273.8	33.0	723	9	US-10-151-882-9	Sequence 9, Appli
44	272.6	32.8	756	9	US-10-237-667-17	Sequence 17, Appli
45	272.6	32.8	756	9	US-10-237-708-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1

US-09-978-752-22

; Sequence 22, Application US/09978752

; Patent No. US20020150559A1

; GENERAL INFORMATION:

; APPLICANT: Mark de Boer

; APPLICANT: Marcel Theodoros

; TITLE OF INVENTION: Induction of T cell tolerance with

; FILE REFERENCE: 99-1

; CURRENT APPLICATION NUMBER: US/09/978,752

; PRIOR FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/235,073

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-21

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/NL97/00438

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-23

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 22

; LENGTH: 879

; TYPE: DNA

; ORGANISM: human

US-09-978-752-22

Query Match 61.5%; Score 510.8; DB 10; Length 879;

Best Local Similarity 80.1%; Pred. No. 4.8e-154;

Matches 634; Conservative 0; Mismatches 137; Indels 21; Gaps 2;

QY 46 GCGGCCCATTCGCTTTGGGGCGGTTCAACTGCACAGCTCTGGGCTGAGCTGCTGAGG 105

DB 46 GCGGCCCATTCGCTTTGGGGCGGTTCAACTGCACAGCTCTGGGCTGAGCTGCTGAGG 105

QY 106 CTGGGGCTTCACTGACGCTGTCTCTCAAGGCTTCGGGCTACACATTTACTGACTATGAA 165

DB 106 CTGGGGCTTCACTGACGCTGTCTCTCAAGGCTTCGGGCTACACATTTACTGACTATGAA 165

QY 166 ATACACTGGGTGAGGACACACCTGTGCATGGCTTGAATGGAGCTATTGATCTT 225

DB 166 ATCAACTGGGTGAGGACACACCTGTGCATGGCTTGAATGGAGCTATTGATCTT 225

QY 226 GAAACTGGTGTACTCCCTACATACAGAGTTCAAGGACAGCCATGACTGTAGAC 285

DB 226 GAAACTGGTGTACTCCCTACATACAGAGTTCAAGGACAGCCATGACTGTAGAC 285

Db 226 TACTATGGTGGTACTAGTTAAATCAGAAGTTCAAGGCAAGGCCACATTGACTGTAGAC 285  
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 Db 286 AAATCTCTCCAGCAGCAGCTTACATGGAGCTCCGAGCCTGACATCTGAAGACTCTGCGCTC 345  
 Qy 346 TATTACTATCAAGATGGTTTGGAGACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 405  
 Db 346 TATTCTGTGCAAGATGGGACTATAGGTACGACGACGGGAGGCTTACTATGTATGGAC 405  
 Qy 406 GAGGGTAAATCTCAGGATCTGGCTCGAATCCAAACCCGG-----GGATGTGTG 456  
 Db 406 TTCTGGGGCCAAAGGACCCAGGCTCAGCGTCTCTCAGCGGTGGCGGATCGGACATTGAG 465  
 Qy 457 ATGACCCCAAAACCCACTCTCCCTGCGCTGTGAGTCTGAGTCAAGCTCAAGCTTCCATCTCTTGC 516  
 Db 466 CTCACTAGTCTCACTCTCCCTGCGCTGTGAGTCTGAGTCAAGCTTCCATCTCTTGC 525  
 Qy 517 AGATCTAGTCAAGCTCTTACAGTAATGGAATCACTTATTTACATTTGGTACCTGCGAG 576  
 Db 526 AGATCTAGTCAAGCTCTTGAACAGTAATGGAATCACTTATTTACATTTGGTACCTGCGAG 585  
 Qy 577 AAGCCAGGCGAGTCTCAAGCTCTGATCTCAAAAGTTTCCAAAGTTTCTGGGGTC 636  
 Db 586 AAGCCAGGCGAGTCTCAAGCTCTGATCTCAAAAGTTTCCAAAGTTTCTGGGGTC 645  
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 Qy 697 GAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTCAAGTCTGCTGATCTCAAG 804  
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 Qy 757 GGAGGGGGACCAAGCTGGAATATA-----AGAGAAAACTCATCTCAGAA 804  
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 Qy 805 GAGGATCTGAAT 816  
 Db 826 GAGGATCTGAAT 837

RESULT 2  
 US-09-203-958-2  
 ; Sequence 2, Application US/09203958  
 ; Publication No. US20030039641A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tibor Keller, et al.  
 ; TITLE OF INVENTION: CELLS EXPRESSING ANTI-Fc RECEPTOR BINDING COMPONENTS  
 ; FILE REFERENCE: MXI-099  
 ; CURRENT APPLICATION NUMBER: US/09/203,958  
 ; CURRENT FILING DATE: 1998-12-02  
 ; EARLIER APPLICATION NUMBER: 60/067,232  
 ; EARLIER FILING DATE: 1997-12-02  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1135  
 ; TYPE: DNA  
 ; ORGANISM: synthetic construct  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (74)..(1132)  
 US-09-203-958-2

Query Match 50.5%; Score 419.4; DB 9; Length 1135;  
 Best Local Similarity 72.0%; Pred. No. 1.4e-124;  
 Matches 588; Conservative 0; Mismatches 196; Indels 33; Gaps 2;  
 Qy 43 GCGGCGGCGGATCTGCGCTTGGCGGCTTCAAGTCAAGGAGTCTGGGCTGAGCTGGTG 102  
 Db 161 GCTGGGCGGCGGCGGCGGATCTGAGATCCAGCTGCGGAGTCTGAGCTGGTG 220

Qy 103 AGGCTGGGGCTTCAAGTCAAGGCTTCCGAGCTACACATTTACTGACTAT 162  
 Db 221 AAGCTGGGGCTTCAAGTCAAGGCTTCCGAGCTTCTGGTATTCATCTGACTAT 280  
 Qy 163 GAAATACACTGGGTGAGGCGAGACACTGTGCGATGCGCTGGAAATGGATTGGAGCTATTGAT 222  
 Db 281 ATCATATTTGGGTGAAGCAGAGCCATGGAAGAGCCTTGAAGTGGACTGGAATAATAAT 340  
 Qy 223 CCTGAAATCTGGGTGAGTCCCTTACAAATCAGAGTTTCAAGGCAAGGCCATAGTACTGTA 282  
 Db 341 CCTTACTAGTGTAGTACTAGTACAAATCTGAAGTTTCAAGGCAAGGCCATAGTACTGTA 400  
 Qy 283 GACAAATCTCCAGCACAGCCTTACATGAGCTCCGAGCTCCAGCTCAGCATCTGAAGACTCTGCC 342  
 Db 401 GACAAATCTCCAGCACAGCCTTACATGAGCTCAGCATCTGAGACTCTGCA 460  
 Qy 343 GTCTATTACTATACAAGATG-----GTTTGGAGGAC 372  
 Db 461 GTCTATTACTGTGAAGAGGAGTTTATTACTACGGTAGTAGCTACGAGGCTTCTCTTAC 520  
 Qy 373 TGGGGCCAGGAGCTCTGCTCACTCTCTGCGAGGGT---AAATCTCTCAGGACTCTGCC 429  
 Db 521 TGGGGCCAGGAGCTCTGCTCACTCTCTGCGAGGGTGGCGCTCCGAGGAGGTGGC 580  
 Qy 430 TCCGAATCCAAACCCGGGATGTTGTGATGACCCCAACCCACTCTCCCTGCTGTCACT 489  
 Db 581 ACCGAGGGGGCGGATCCGATGTTGTGATGACCCAGACTCCACTCACTTTGTGATACC 640  
 Qy 490 CTGGAGATCAAGCTCCATCTTTGCGAGATCTAGTCAAGCCTTTTACAGAGTAAATGGA 549  
 Db 641 ATTGACAAACAGCCTCCATCTCTTGAAGTCAAGTCAAGCTCAGAGCTCTTAGATAGTATGA 700  
 Qy 550 ATCACTATTTACATGTTGTTACCTGCGAGAGCCAGGCTCTCCAAAGCTCTGATCTAC 609  
 Db 701 AAGACATATTTGAATTTGTTTACAGAGGCGGAGCTCTCCAAAGCTCTGATCTAT 760  
 Qy 610 AAAGTTTCAACCGGATTTCTGGGGTCCAGACAGCTTCAAGTGGCAGTGGATCAGGGACA 669  
 Db 761 CTGGTGTCTAACTGGACTCTGGAGTCTCTGACAGTTTCACTGGCAGTGGATCAGGGACA 820  
 Qy 670 GATTTCACTCAAGATCAGCAGAGTGGAGCTGAGGATCTGGGAGTTTATTTCTGCTCT 729  
 Db 821 GATTTCACTCAAGATCAGCAGAGTGGAGCTGAGGATTTGGGAATTTATTTCTGCTGG 880  
 Qy 730 CAAAGTACACATGTTCCGTACACGTTCCGAGGGGGGAGCCAGCTGGAATAAAGAGNA 789  
 Db 881 CAAAGTACACATTTCTCTCAGACGTTCCGAGGGGAGCCAGCTGGAATCAACCGCGG 940  
 Qy 790 AAATCTCATCTCAGAGAGGATCTGAATTTAGTAAGCGG 826  
 Db 941 CTGAGGTCGAGCAAACTCATCTCAGAGAGG 977

RESULT 3  
 US-09-968-851-46  
 ; Sequence 46, Application US/09968851  
 ; Publication No. US20020193561A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CONSEILLER, EMMANUEL  
 ; BRACCO, LAURENT  
 ; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
 ; USES THEREOF  
 ; NUMBER OF SEQUENCES: 59  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
 ; DUNN, LLP  
 ; STREET: 1300 I Street, NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3315  
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT: US/09/968.851  
FILING DATE: 03-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/983.035  
FILING DATE: 20-Feb-1998  
APPLICATION NUMBER: PCT/FR96/01111  
FILING DATE: 17-JUL-1996  
APPLICATION NUMBER: FR 95/08729  
FILING DATE: 19-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Strauss, William L.  
REGISTRATION NUMBER: 47,114  
REFERENCE/DOCKET NUMBER: 03804.0142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4000  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 749 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-968-851-46  
Query Match 49.1%; Score 407.6; DB 9; Length 749;  
Best Local Similarity 74.1%; Pred. No. 7.3e-121;  
Matches 547; Conservative 0; Mismatches 179; Indels 12; Gaps 2;

QY 58 GCCTTTGGGGGTTCAACTGCGAGCTCTGGGCTGAGCTGGTGAGCCCTGGGGCTTCA 117  
DB 1 GCCATGGCCCGAGGTGACCTGCGAGTTCAGGGGCGAGGCTTGGGGTCAAGGCGCTCA 60  
QY 118 GTGAGCTGTCTGCAAGGCTTCGGGCTACACATTTACTGACTATGAATACACTGGGTG 177  
DB 61 GTCAGTTGCTGCGACAGCTTCGGCTTCAACATTAAGACTACTATGCACTGGGTG 120  
QY 178 AGGCAGACACCTGTGATGGCTGGAATGATGGAGCTATTGATCTGAACTGGTGGT 237  
DB 121 AAGCAGAGGCTGGAACAGGCTGAGATGGATGATGATGATGATGATGATGATGAT 180  
QY 238 ACTGCTACATCAGAAGTTCAAGCAAGGCCATAGTACTGTAGACAAATCCTCCAGC 297  
DB 181 ACTGAATATGCCCGAAGTTCCAGGCAAGGCCACTATGACTGCAGACACATCCTCCAAT 240  
QY 298 ACAGCTACATGGAGTCCGAGCTGACATCTGAAGACTCTGCGCTTATTACTATACA 357  
DB 241 ACAGCTACCTGAGCTCAGAGCTGACATCTGAGGACTGCGCTTATTATTGTAAT 300  
QY 358 AGAT-----GGTTGAGACTGGGGCCCAAGGACTCTGGTCACTGTCTGCGCAGAG 408  
DB 301 TTTTACGGGGATGCTTTGGACTACTGCGGCGCAAGGACCACGGTCTCTCCTCAGGT 360  
QY 409 GGTAAATCCTCA---GGATCTGGCTCCGAATCCAAACCCGGGGATGTTGATGACCCCA 465  
DB 361 GGAGCGGTTTCAGGCGGAGGTGGTCTGCGCGTGGCGGATCGGATGTTTGTATGACCCAA 420  
QY 466 AACCACTCTCCCTGCTGCTGCTGCTGAGATCAAGCTCCTCTCTTGCAGATCTAGT 525  
DB 421 ACTCACTCACTTGTTCGGTACCATTGGAAACACAGGCTCCTCACTCTTGAAGTCAAGT 480  
QY 526 CAGAGCCTTTTACACAGTAATGGAATACCTATTATTTACATTTGATCTGCAGAACCGGC 585  
DB 481 CAGAGCCTTTTGGATAGTGGGAAGACATATTGATTTGGTTTACAGAGGCGCAGGC 540  
QY 586 CAGTCTCAAAAGCTCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGGTCCCAGACAGG 645

DB 541 CAGTCTCAAAAGCGCCTAATCTATCTGGTGTCTAAACTGCACTCTGGAGTCCCTGACAGG 600  
QY 646 TTCAGTGGCAGTGGATCAGGACAGATTTTTCACACTCAAGATCAGCAGAGTGGAGGCTGAG 705  
DB 601 TTCAGTGGCAGTGGATCAGGACAGATTTTTCACACTCAAGATCAGCAGAGTGGAGGCTGAG 660  
QY 706 GATCTGGGAGTTTATTCTGCTCTCAAGTACACATGTTCCGTACACAGTTCCGAGGGGG 765  
DB 661 GATTTGGGAGTTTATTCTGCTGGCAAGGTACACATTTCTCCGCTCACGTTCCGTTGGTGGG 720  
QY 766 ACCAAGCTGGAATAAAA 783  
DB 721 ACCAAGCTGGAGCTGAAA 738  
RESULT 4  
US-09-968-851-37  
Sequence 37, Application US/09968851  
Publication No. US20020193561A1  
GENERAL INFORMATION:  
APPLICANT: CONSEILLER, EMMANUEL  
BRACCO, LAURENT  
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
DUNNER, LLP  
STREET: 1300 I Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/968.851  
FILING DATE: 03-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/983.035  
FILING DATE: 20-Feb-1998  
APPLICATION NUMBER: PCT/FR96/01111  
FILING DATE: 17-JUL-1996  
APPLICATION NUMBER: FR 95/08729  
FILING DATE: 19-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Strauss, William L.  
REGISTRATION NUMBER: 47,114  
REFERENCE/DOCKET NUMBER: 03804.0142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1611 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1605  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-968-851-37  
Query Match 48.8%; Score 405.2; DB 9; Length 1611;  
Best Local Similarity 74.1%; Pred. No. 5.9e-120;  
Matches 544; Conservative 0; Mismatches 178; Indels 12; Gaps 2;



; PRIOR FILING DATE: 2000-07-03  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 4661  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-897-006-10

Query Match 42.3%; Score 351.4; DB 10; Length 4661;  
Best Local Similarity 70.7%; Pred. No. 1.9e-102;  
Matches 514; Conservative 0; Mismatches 201; Indels 12; Gaps 3;

Qy 69 GTTCAACTGACAGAGCTGGGGCTGAGCTGTGAGGCTGGGGCTTCAGTGACGCTGTC 128  
Db 2157 GGTTCAGTTGCAGCAGCTGACGCTGAGTTGGTGAACCTGGGGCTTCAGTGAAGATTTC 2216  
Qy 129 CTGCAAGGCTTGGGCTACATTTACTGACTATGAATAATACACTGGGTGAGGCAGACACC 188  
Db 2217 CTGCAAGGCTTCTGGCTACACTTCACTGACCATGCAATTCAGTGGTGAACAGAACCC 2276  
Qy 189 TGTGCATGGCCTGGATGGATTGGAGCTATTGATCCTGAACTGGTGTACTGCTACAA 248  
Db 2277 TGAACAGGGCTGGAAATGGATTGGATATTTTCTCCCGAAATGATTTTAAATCAA 2336  
Qy 249 TCAGAAGTTCAAGACAAGGCGCATAGTGAATCTAGACAAATCCTCCAGCAGACCTACAT 308  
Db 2337 TGAGAGTTCAAGGCGAGGCGACACTGACTGCAGACAAATCCTCCAGCAGTGCCTAGT 2396  
Qy 309 GGAGTCCGAGCCTGACATCTGAAGATCTTGCCTGTCTATTACTATACAAGT-----G 362  
Db 2397 GCAGCTCAACAGCCTGACATCTGAGGATTTCTGAGTGTATTCTGTACAAGATCCCTGAA 2456  
Qy 363 GTTTCAGGACTGGGCGCAGGAGCTCTGGTCACTGTCTCTGAGAGGGTAAA---TCTC 419  
Db 2457 TATGGCCTACTGGGGTCAAGGAACCTCAGTCAACGCTCTCCTCAGGAGGGGAGGAGCGG 2516  
Qy 420 AGGATCTGGCTCCGAATCCAAACCCGGGGATGTTGTGATGACCCCAACCCACTCTCCCT 479  
Db 2517 AGGCGGTGGCTCGGAGGGGAGGCTCGGACATGTGATGTACAGTCTCCATCTCCCT 2576  
Qy 480 GCCTGTAGTCTTGAGATCAAGCCTCCATCTCTTTCAGATCTAGTCAAGCCTTTTACA 539  
Db 2577 ACCTGTGCTGAGTGGCGAAGAGTTACTTTGAGCTGCAAGTCCAGTCAAGACCTTTTATA 2636  
Qy 540 CA---GTAATGGAATCACTATTTACATTTGGTACCTGAGAGCCAGGCCAGTCTCCAAA 596  
Db 2637 TAGTGGTAAATCAAAAGAACTACTTGGCCTGGTACCAGAGAAACAGGGCAGTCTCTTAA 2696  
Qy 597 GCTCTGATCTACAAAGTTTCCAAACCGGATTTTCTGGGCTCCAGACAGGTTCAAGTGGCAG 656  
Db 2697 ACTGCTGATTTACTGGGATCCGCTAGGGAATCTGGGTCTCCTGATCCCTTCAGGGCAG 2756  
Qy 657 TGGATCAGGACAGATTTTCACTCAAGATCAGAGATGAGGCTGAGGATCTGGGAGT 716  
Db 2757 TGGATCTGGACAGATTTTCACTCTCTCCATCAGCAGTGAAGACTGAAGACCTGGCAGT 2816  
Qy 717 TTATTTCTGCTCTCAAGTACACATGTTCCCGTACACGTTCCGAGGGGGAGCCAGCTGGA 776  
Db 2817 TTATTTCTGTCAGCAGTATTATAGCTATCCCTCAGTTTCCGTTGCTGGGACCAAGCTGGT 2876  
Qy 777 AATAAAA 783  
Db 2877 GCTGAAA 2883

RESULT 7  
US-09-924-099-20  
; Sequence 20: Application US/09924099  
; Patent No. US20020128450A1  
; GENERAL INFORMATION:

; APPLICANT: NISHIDA, Yoshihiro  
; APPLICANT: OKURA, Takanori  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PEPTIDE  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/924,099  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 33  
; SEQ ID NO 20  
; LENGTH: 729  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of  
; OTHER INFORMATION: SEQ  
; OTHER INFORMATION: ID NO:10  
US-09-924-099-20

Query Match 40.2%; Score 334; DB 10; Length 729;  
Best Local Similarity 68.3%; Pred. No. 3.6e-97;  
Matches 504; Conservative 0; Mismatches 210; Indels 24; Gaps 2;

Qy 67 GCGGTTCAACTGACAGCAGTCTGGGGCTGAGCTGGTGGAGCCTGGGGCTTCAGTGACGCTG 126  
Db 1 GAGATCCAGCTGACAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGTTC 60  
Qy 127 TCCTGCAAGGCTTCGGGCTACACATTTTACTGACTATGAAATATACACTGGGTGAGCAGACA 186  
Db 61 TCCTGTAAGGCTTCGGTACTCATTCAGTCACTGACTACTTCATTTCGGTGAACGAGCAGC 120  
Qy 187 CTTGTGATGCCCTGGAAATGGATTGGAGCTATTGATCCTGAAACTGGTGTACTGCCCTAC 246  
Db 121 CATGAAAGAGCCTTGGATGGATTGGAGATTTGATCCTTATATGTTGATAGTTAGTTAC 180  
Qy 247 AATCAGAAGTTCAAGGACAAGGCCATAGTCACTGATAGCAAAATCCTCCAGCAGCAGCTAC 306  
Db 181 AACAGAAGTTTCAGGACAAGGCCACATTCAGTCTTGACCAGTCTCCACACAGCCTTC 240  
Qy 307 ATGAGAGTCCGCGAGCCTGACATCTGAAAGACTCTGCCCTCTATTACTATACAAGATGGTTT 366  
Db 241 ATGCATCTCAACAGCCTGACATCTGAGGACTCTGCACTCTATTCTGTGCAAGAGGCTTA 300  
Qy 367 GAGGACTGGGGCCAAAGGAGCTCTGGTCACTGTCTCTGCA-----GAGGGTAAATCC 417  
Db 301 CGGTTCTGGGGCCAAAGGAGCTCTGGTCACTGTCTCTGAGGTGGAGGTGGAGCGGATCC 360  
Qy 418 TCAGGATCTGGCTCCGAATCCAAACCCGGGGATGTTGTGATGACCCCAACCCACTCTCC 477  
Db 361 GGGGAGGTGGCTCTGGGGTGGCGGATTCGGACATCCAGATGACCCAGTCTCCATCTCC 420  
Qy 478 CTGCTGTGAGTCTTGAGATCAAGCCTCCATCTCTTTCAGATCTAGTCAAGAGCCTTTTA 537  
Db 421 TTATCTGCTCTCTGGGAGAAAGAGTCACTCTCACTGTCTGGGCAAGTCAAGACATT--- 477  
Qy 538 CACAGTAATGGAATCACTATTATACATTGTTGATCTGAGAAAGCCAGGCCAGTCTCCAAAG 597  
Db 478 -----GGTAGTAAATTTATCTGCTTCAACAGGAACCCAGATGGAACCTTTTAA 525  
Qy 598 CTCTGATCTACAAAGTTTCCAAACCGATTTCCTGGGGTCCAGACAGGTTTCAGTGGCAGT 657  
Db 526 CGCCTGATCTACGCCACATCCAGTTTAGATTCTGGGTGCTCCCAAGAGGTTTCAGTGGCAGT 585  
Qy 658 GGATCAGGAGCAGATTTTCACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTT 717  
Db 586 AGGTCTGGGTGAGATTTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGAC 645



QY 718 TATTCTGCTCTCAAGTACACATGTTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAA 777  
| | | | |  
Db 646 TATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGCA 705  
| | | | |  
QY 778 ATAAAGAGAAAAAATC 795  
| | | | |  
Db 706 ATAAACATCAACCATCAC 723  
| | | | |

## RESULT 8

US-09-924-099-19  
; Sequence 19, Application US/09924099  
; Patent No. US20020128450A1  
; GENERAL INFORMATION:  
; APPLICANT: NISHIDA, Yoshihiro  
; APPLICANT: OKURA, Takanori  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PEPTIDE  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/924,099  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 33  
; SEQ ID NO 19  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of  
; OTHER INFORMATION: SEQ  
; OTHER INFORMATION: ID NO: 9  
US-09-924-099-19

Query Match 40.1%; Score 333.2; DB 10; Length 711;  
Best Local Similarity 68.7%; Pred. No. 6.4e-97;  
Matches 499; Conservative 0; Mismatches 203; Indels 24; Gaps 2;  
  
2Y 67 GCGGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCTGGGGCTTCAGTGACGGTG 126  
| | | | |  
2b 1 GAGATCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCTGGGGCTTCAGTGAAGTTC 60  
| | | | |  
2Y 127 TCTGCAAGCTTCGGGCTACACATTTACTGACTATGAATACATCACTGGGTGAGGCAGACA 186  
| | | | |  
2b 61 TCCTGTAAGGCTTCGGTTACTCACTCACTGACTTCTTACTTTACTGGTGAAGCAGAGC 120  
| | | | |  
2Y 187 CTTGTGTCATGCGCTGGAATGATTGGAGCTATTGATCTTCAAACTGGTGTACTGCCTAC 246  
| | | | |  
2b 121 CATGGAAGAGCTTGAGTGATGGAGATATTGATCTTATATGATGATAGTACTAGTTAC 180  
| | | | |  
2Y 247 AATCAGAAGTTCAAGGACAAAGGCATAGTACTGTAGACAAATCTCCAGCACAGCCTAC 306  
| | | | |  
2b 181 AACCAAGAAGTTCAAGGACAAAGGCACATTCAGTGTGGACAGCTCCCTCCACACAGCCTTC 240  
| | | | |  
2Y 307 ATGAGCTCCGAGCTGACATCTGAAGATCTGCGCTCTATTACTATACAAAGATGGTTT 366  
| | | | |  
2b 241 ATGATCTCAACAGCTGACATCTGAGGACTCTGCAGTCTATTCTGTGCAAGAGGCCTA 300  
| | | | |  
2Y 367 GAGGACTTGGGCAAGGAGCTCTGGTCACTGTCTCTGCA-----GAGGGTAAATCC 417  
| | | | |  
2b 301 CGGTTCTGGGGCAAGGAGCTCTGGTCACTGTCTCTGAGAGTGGAGGCGGATCC 360  
| | | | |  
2Y 418 TCAGGATCTGGCTCCGAATCCAAACCCGGGAGTGTGTGATGACCCCAACCCACTCTCC 477  
| | | | |  
2b 361 GCGGAGGTGGCTCTGGCGGTGGCGATCGACATCGAGATGACCCAGCTCTCCATCTCC 420  
| | | | |  
2Y 478 CTGCTGTGAGTCTTGGAGATCAAGCCTCCATCTCTTTGAGATCTTAGTCAGAGCCTTTTA 537  
| | | | |

Db 421 TTATCTGCCTCTCTGGAGAAAGAGTCAGTCTCACTTGTTCGGCAAGTCAGGACATTC-- 478  
| | | | |  
QY 538 CACAGTAATGGAATCACCTATTATACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAG 597  
| | | | |  
Db 479 -----GTAGTAATATATAGTGGCTTCAACAGGAACCATGATGGAACCTTTTAA 525  
| | | | |  
QY 598 CTCCTGATCTACAAAGTTTCCAAACCGATTTTCGGGGTCCACAGAGGTTTCAGTGGCAGT 657  
| | | | |  
Db 526 CGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAGAGGTTTCAGTGGCAGT 585  
| | | | |  
QY 658 GGATCAGGACAGATTTACACTCAAGATCAGAGTCAGAGCTGAGGATCTGGAGTT 717  
| | | | |  
Db 586 AGGTCTGGGTGAGATTATTTCTCTCCATCAGCAGCCTTAGTCTCAAGATTTTGTAGAC 645  
| | | | |  
QY 718 TATTCTGCTCTCAAAAGTACACATGTTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAA 777  
| | | | |  
Db 646 TATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGCA 705  
| | | | |  
QY 778 ATAAAA 783  
| | | | |  
Db 706 ATAAAA 711  
| | | | |

## RESULT 9

US-10-060-585-6  
; Sequence 6, Application US/10060585  
; Publication No. US20030083290A1  
; GENERAL INFORMATION:  
; APPLICANT: Kingsman, Alan J.  
; APPLICANT: Bebbington, Christopher R.  
; APPLICANT: Carroll, Miles W.  
; APPLICANT: Ellard, Fiona M.  
; APPLICANT: Kingsman, Susan M.  
; APPLICANT: Myers, Kevin A.  
; TITLE OF INVENTION: VECTOR SYSTEM  
; FILE REFERENCE: DYOU23.00ICPI  
; CURRENT APPLICATION NUMBER: US/10/060,585  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 09/445375  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: GB 9711579.4  
; PRIOR FILING DATE: 1997-06-04  
; PRIOR APPLICATION NUMBER: GB 9713150.2  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: GB 9714230.1  
; PRIOR FILING DATE: 1997-07-04  
; PRIOR APPLICATION NUMBER: PCT/GB00/04317  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: PCT/GB99/03859  
; PRIOR FILING DATE: 1999-11-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 2090  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 514 ScFv - human IgE fusion  
US-10-060-585-6

Query Match 38.7%; Score 321; DB 9; Length 2090;  
Best Local Similarity 67.1%; Pred. No. 8.3e-93;  
Matches 519; Conservative 0; Mismatches 215; Indels 39; Gaps 3;  
  
QY 35 TTTTCGGCGCGCGCGCATTCCTGCTTTGCGCGGTTCAACTGCAGCAGTCTGGGGCTG 94  
| | | | |  
Db 37 TCTTGTAGCAACACATACAGGTGTCCACTCCGAGGTCCAGCTGCAGCAGTCTGGACCTG 96  
| | | | |  
QY 95 AGCTGGTAGGCTCGGGCTTCAGTGACGCTCTCTGCAAGGCTTCGGGCTACACATTTA 154  
| | | | |  
Db 97 ACCTGGTAGGCTCGGGCTTCAGTGAAGATATCTGCNAGGCTTCTGGTACTATTCA 156  
| | | | |  
QY 155 CTGACTATGAATAATACATGGGTGAGGCGACACCTGTGATGCGCTGGAATGGATTGGAG 214  
| | | | |

157 CTGGCTACTACATGCTGGTGAAGCAGAGCCATGAAAGAGCCTTGGTGGATTGGAC 216  
215 CTATTGATCTGAACTGGTGGTACTGCTACATCAGAAAGTTCAAGCACAAGCCATAG 274  
217 GTATTATCTTAACTGGTGGTACTCTTACACACAGAAATTCAGGACAGGCCATAT 276  
275 TGACTGTAGACAAATCTCCAGCAGACGCTTACATGGAGTCCGAGCCTGACATCTGAAG 334  
277 TAACGTGTAGACAAGTATCACCACAGCCTACATGGAGTCCGAGCCTGACATCTGAGG 336  
335 ACTCTGCGGTCTATTACTATACAGAT-----GGTTGAGACT 373  
337 ACTCTGCGGTCTATTACTGTGAAGATCTACTATGATTCAGAACTATGTTATGACTACT 396  
374 GGGCCCAAGGACTCTGGTCACTCTCTCTGAGAGGGTAAATCTCAGGATCTGGCTCCG 433  
397 GGGGTCAAGTAACTTCACTCAGTCACTCTCTTCAAGTGGTGGAGCGGTGGTGGCGCA 456  
434 AATCAAACCCGG---GGATGTTGTGATGAGCCCAACCCACTCTCCCTGCTGTGATC 490  
457 CTGCGCGGGCGGATAGTATTGTGATGAGCCCAAGCTCCACATCTCTGCTGTTTTCAG 516  
491 TTGAGATCAAGCCTCCTCTCTGAGATCTAGTCAAGCCTTTTACACAGTAATCGAA 550  
517 CAGGAGCAGGGTTACCATACCTGCAAGGCCAGTCAG-----TGTA 561  
551 TCACCTATTTACATTTGATGCTGAGAGCCAGGCCAGTCTTCCAAAGCTCTGATCTACA 610  
562 GTAATGATGATGTTGTACCAAGAGCCAGGGCAGTCTCTACATGCTCATATCCT 621  
611 AAGTTTCCAAACCGATTTCTGGGTCCAGACAGGTTCAAGTGGCAGTGGATCAGGACAG 670  
622 ATACATCCAGTCGCTGCTGAGTCCCTGATGCTCTCATTTGGCAGTGGATCGGACGG 681  
671 ATTTCACTCAAGATCAGCAGATGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTC 730  
682 ATTTCACTTTCCACATCAGCACTTTGCAAGGCTGAAGACCTTGTCTGTCAGC 741  
731 AAAGTACACATGTTCCGTACACGTTTGGAGGGGGGACCAAGCTGGAATAAAA 783  
742 AAGATTATATTTCTCTCCGAGGTTGGTGGAGCCACCAAGCTTGAATCAAA 794

RESULT 10  
US-09-753-436-44  
; Sequence 44, Application US/09753436  
; Patent No. US20010029293A1  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Vazeux, Rosemay  
; TITLE OF INVENTION: ICAM-Related Materials and Methods  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09753.436  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/382,289  
; FILING DATE:  
; APPLICATION NUMBER: US 08/487,113

; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,754  
; FILING DATE: 05-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/102,852  
; FILING DATE: 05-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/009,266  
; FILING DATE: 22-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/894,061  
; FILING DATE: 05-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/889,724  
; FILING DATE: 26-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,689  
; FILING DATE: 27-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Joseph A., Jr.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 33282  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 384 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-753-436-44

Query Match 38.6%; Score 320.4; DB 10; Length 384;  
Best Local Similarity 96.7%; Pred. No. 6.5e-93;  
Matches 327; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 446 GGATGTTGTGATGACCCCAACCCACTCTCCCTGCTGTGCTGAGTCAAGCCT 505  
DB 47 GTGACCTGTGATGACCCCAACCTCACTCTCCCTGCTGTGCTGAGTCAAGCCT 106  
QY 506 CCATCTCTTGCAGATCTAGTCAGAGCCTTTTACACAGTAATGAAATCACTATTACAT 565  
DB 107 CCATCTCTTGCAGATCTAGTCAGAGCCTTTGTACACAGTAATGAGACACCTATTACAT 166  
QY 566 GTACCTGCAGAAAGCCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGAT 625  
DB 167 GGTACCTGCAGAAAGCCAGGCCAGTCTCCACAGCTCTGATCTACAAAGTTTCCAAACCGAT 226  
QY 626 TTCTCGGGTCCAGACAGGTTCCAGTGGCAGTGGATCAGGACAGATTTTCCACTCAAGA 685  
DB 227 TTCTCGGGTCCAGACAGGTTCCAGTGGCAGTGGATCAGGACAGATTTTCCACTCAAGC 286  
QY 686 TCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAAGTACATGTTTC 745  
DB 287 TCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAAGTACATGTTTC 346  
QY 746 CGTACACGTTTCGAGGGGGGACCAAGCTGGAATAAAA 783  
DB 347 CGTACACGTTTCGAGGGGGGACCAAGCTGGAATAAAA 384

RESULT 11  
US-09-518-737-3  
; Sequence 3, Application US/09518737  
; Publication No. US20030008321A1  
; GENERAL INFORMATION:  
; APPLICANT: FUKUI, YASUHIKA  
; APPLICANT: NAGATA, SATOSHI  
; APPLICANT: SHIRAI, RYUICHI

APPLICANT: SAITO, NAOKI  
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING  
FILE REFERENCE: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE  
CURRENT APPLICATION NUMBER: US/09/518,737  
CURRENT FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: JP 1999-250209  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 336  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(336)  
US-09-518-737-3

Query Match 38.6%; Score 320; DB 9; Length 336;  
Best Local Similarity 97.0%; Pred. No. 8.3e-93;  
Matches 326; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 448 GATGTTGTGATGACCCCAACCACTCTCCCTGCTGTCAGTCTTGGAGATCAAGCCTCC 507  
Db 1 GATGTTGTGATGACCCCAACCACTCTCCCTGCTGTCAGTCTTGGAGATCAAGCCTCC 60

QY 508 ATCTCTGTCAGATCTAGTCAGAGCCTTTTACACAGTAATGGAATACACCTATTACATGG 567  
Db 61 ATCTCTGTCAGATCTAGTCAGAGCCTTTTACACAGTAATGGAATACACCTATTACATGG 120

QY 568 TACCTGACAGAGCCAGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATT 627  
Db 121 TACCTCCAGAAACAGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATT 180

QY 628 TCTGGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATC 687  
Db 181 TCTGGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATC 240

QY 688 AGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCG 747  
Db 241 AGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCG 300

QY 748 TACACGTTCCGAGGGGGACCAAGCTGGAAATAAAA 783  
Db 301 TACACGTTCCGAGGGGGACCAAGCTGGAAATAAAA 336

RESULT 12  
US-10-060-585-5  
Sequence 5, Application US/10060585  
Publication No. US20030083290A1  
GENERAL INFORMATION:  
APPLICANT: Kingseman, Alan J.  
APPLICANT: Bebbington, Christopher R.  
APPLICANT: Cartoll, Miles W.  
APPLICANT: Ellard, Fiona M.  
APPLICANT: Kingseman, Susan M.  
APPLICANT: Myers, Kevin A.  
TITLE OF INVENTION: VECTOR SYSTEM  
FILE REFERENCE: DYOU23.004CP1  
CURRENT APPLICATION NUMBER: US/10/060,585  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US 09/445375  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: GB 9711579.4  
PRIOR FILING DATE: 1997-06-04  
PRIOR APPLICATION NUMBER: GB 9713150.2  
PRIOR FILING DATE: 1997-06-20  
PRIOR APPLICATION NUMBER: GB 9714230.1  
PRIOR FILING DATE: 1997-07-04  
PRIOR APPLICATION NUMBER: PCT/GB00/04317  
PRIOR FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: PCT/GB99/03859  
PRIOR FILING DATE: 1999-11-18  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 1518  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: B7 link ScFv sequence  
US-10-060-585-5

Query Match 38.5%; Score 319.4; DB 9; Length 1518;  
Best Local Similarity 66.8%; Pred. No. 2.4e-92;  
Matches 535; Conservative 0; Mismatches 226; Indels 40; Gaps 4;

QY 7 ATGGTAAGGCTATTGTTTATATGCTTTTGGCGGGCGCGGCATCTCGCTTTGGG 66  
Db 728 ATAGCAAGCCCGGGGTGGTGGAGCGGTGGTGGCGGCGGCGGCGGAAGTAG-T 786

QY 67 GCGGTTCAACTGCACAGCTCTGGGCTGAGCTGGTGGAGCCTGGGCTTCAGTGACGCTG 126  
Db 787 GAGTCCAGCTTCACAGCTTGGACCTGACCTGGTGAAGCCTGGGCTTCAGTGAAGATA 846

QY 127 TCTGCAAGGCTTCGGGCTACACATTTACTGACTATGAATACACTGGGTGAGGAGACA 186  
Db 847 TCTGCAAGGCTTCGGTACTCACTGCTACTACATGCACTGGGTGAAGCAGAGC 906

QY 187 CTTGTGCATGGCTCGGAATGGATTGGAGCTATTGATCTGAAACTGGTGGTACTGCCTAC 246  
Db 907 CATGGAAGAGCGCTTGAGTGGATTGAGCTATTAACTCTAACTGTTTACTCTCTAC 966

QY 247 AATCAAGATTCAAGCAAGCCAGCTAGTGTAGACAAATCTCCAGACACAGCTAC 306  
Db 967 AACCAAAATTCAGGCAAGCCCATATTAATCTGAGACAAAGTATCCACCAAGCTTAC 1026

QY 307 ATGGAGCTCCGAGCCTGACATCTGAAGACTCTGCCGTCTATTACTATACAAGAT- 361  
Db 1027 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGCCGTCTATTACTGTGCAAGATCTACT 1086

QY 362 -----GGTTTGAGCACTGGGCGGCGGCACTGCTGCTCTCTCTGCA 405  
Db 1087 ATGATTACGAATCTGTTATGGACTACTGGGCTCAAGTAACTTCAGTCAAGCTCTCTTCA 1146

QY 406 GAGGCTAAATCTCAGGATCTGGCTCCGAATCCAAACCCGG- -GGATGTTGTGATGACC 462  
Db 1147 GGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGAGTCTAGTATTGTGATGACC 1206

QY 463 CCAAAACCCACTCTCCCTGCTGTCTAGTCTTGGAGATCAAGCCTCCATCTCTTTCAGATCT 522  
Db 1207 CAGACTCCCACTCTCTGCTGTTTTCAGCAGGAGACAGGGTTTACCATAACCTGCAAGGCC 1266

QY 523 AGTCAGAGCCTTTTACACAGTAATGGAATACCTATTATTCATTTGTTACTGTCGAGAGCCA 582  
Db 1267 AGTCAGAG- - - - -TGTGAGTAATGATGTAGCTTGGTACCAACAGAGAGCCA 1311

QY 583 GGCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTTCCTGGGTCCAGAC 642  
Db 1312 GGCAGTCTCTTACACTCTCATATCCTATACATCCAGTCTGCTAGCTGGAGTCCCTGAT 1371

QY 643 AGGTTTCAGTGGCAGTGGATCAGGAGACAGATTTCACACTCAAGATCAGCAGAGTGGAGCT 702  
Db 1372 CGCTTCATTGGCAGTGGATGGAAGCGATTTCCTTTCACCATCAGCACTTTGCGAGCT 1431

QY 703 GAGGATCTGGGAGTTTATTTCTGCTCTCAAGATACACATGTTCCGTACACGTTCCGAGGG 762  
Db 1432 GAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCTCCGACGTTCCGTGGA 1491

QY 763 GGCACCAAGCTGGAAATAAAA 783  
Db 1492 GGCACCAAGCTGGAAATAAAA 1512

RESULT 13  
 US-10-060-585-2  
 ; Sequence 2, Application US/10060585  
 ; Publication No. US20030083290A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kingsman, Alan J.  
 ; APPLICANT: Bebbington, Christopher R.  
 ; APPLICANT: Carroll, Miles W.  
 ; APPLICANT: Eillard, Fiona M.  
 ; APPLICANT: Kingsman, Susan M.  
 ; APPLICANT: Myers, Kevin A.  
 ; TITLE OF INVENTION: VECTOR SYSTEM  
 ; FILE REFERENCE: DYOU23.001CP1  
 ; CURRENT APPLICATION NUMBER: US/10/060,585  
 ; CURRENT FILING DATE: 2002-09-06  
 ; PRIOR APPLICATION NUMBER: US 09/445375  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: GB 9711579.4  
 ; PRIOR FILING DATE: 1997-06-04  
 ; PRIOR APPLICATION NUMBER: GB 9713150.2  
 ; PRIOR FILING DATE: 1997-06-20  
 ; PRIOR APPLICATION NUMBER: GB 9714230.1  
 ; PRIOR FILING DATE: 1997-07-04  
 ; PRIOR APPLICATION NUMBER: PCT/GB00/04317  
 ; PRIOR FILING DATE: 2000-11-13  
 ; PRIOR APPLICATION NUMBER: PCT/GB99/03859  
 ; PRIOR FILING DATE: 1999-11-18  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1807  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: 5T4Sabi  
 US-10-060-585-2  
 Query Match 38.3%; Score 317.8; DB 9; Length 1807;  
 Best Local Similarity 66.9%; Pred. No. 8.4e-92;  
 Matches 517; Conservative 0; Mismatches 217; Indels 39; Gaps 3;  
 QY 35 TTTTGGCGGGCGGCGCATCTTCCTTTGGCGGGTTCACTGCGCAGCAGTCTGGGCGTG 94  
 DB 37 TCTTGGTAGCAACAGCTACAGGTGTCCACTCCGAGGTCCAGCTTCGACAGCTCTGGACCTG 96  
 QY 95 AGCTGGTGAGCGCTGGGGCTTCACTGACGTGTCTTCAAGGCTTGGGCTTACACATTTA 154  
 DB 97 ACTGGTGAAGCTGGGGCTTCACTGAAGATATCTTCAAGGCTTCTGGTTACTCATTTCA 156  
 QY 155 CTGACTGAATAACACTGGGTGAGGAGACACCTGTGCATGCCCTGGAAATGGATTGGAG 214  
 DB 157 CTGGCTACTACATGCACTGGTGAAGCAGAGCCATGAAAGAGCCTTGTGATTGGAC 216  
 QY 215 CTATTGATCTGAACTGGTGTACTCTCCCTACAATGAGAAGTTCAAGGACAAGGCCATAG 274  
 DB 217 GTATTAACTCAAAATGGTGTACTCTCTCAACCAAGAAATCAAGGACAAGGCCATAT 276  
 QY 275 TGACTGTAGACAAATCTCCAGACACAGCTACATGGAGTCCGAGCCTCACATCTGAAG 334  
 DB 277 TAAGTGTAGAACAGTCAATCACCACAGCCTACATGGAGTCCGAGCCTCACATCTGAGG 336  
 QY 335 ACTCTGCGGTCTATTACTATACAAGAT-----GGTTTCAGGACT 373  
 DB 337 ACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATGCAACTATGTTATGCACTACT 396  
 QY 374 GGGGCAAGGACTCTCGTCACTGTCTCTCAGAGGGTAATCTCAGGATCTGGCTCG 433  
 DB 397 GGGGTCAAGTAACCTCAGTCAACCTCTCTCAGTGTGGTGGGAGCGGTGGTGGCGCA 456  
 QY 434 AATCAAAACCGG---GGATCTGTGTGATGACCCCAACCCCACTCTCCCTGCTGTGATC 490  
 DB 457 CTGGCGGCGGCGGATCTAGTATTGTGATGATGCCCACTCCCACTCCCTGCTGTTTTCAG 516

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QY 245 ACAATCAGAGTTCAAGGCAAGCCATAGTACTGTAGACAAATCTCCAGCACAGCCT 304
DB 917 ACAAACCAAAATTCAGGACAGGCCATATTAACTGTAGACAGTCAATCCACACAGCCT 976
QY 305 ACATGGAGCTCCGAGGCTGACATCTGAAGACTCTGGCGTCTATTACTATACAAGAT--- 361
DB 977 ACATGGAGCTCCGAGGCTGACATCTGAGGACTCTGGCGTCTATTACTGTGCAAGATCTA 1036
QY 362 -----GGTTTCAGGACTGGGCGCAAGGACTCTGGTCACTGTCTCTG 403
DB 1037 CTATGATTAGCAACTATTGTATGGACTACTGGGTCAAGTAACTCAGTCACCGTCTCCT 1096
QY 404 CAGAGGTAATCTCAGGACTCTGGCTCCGAATCCAAACCCCGGG---ATGTTGTGATGA 460
DB 1097 CAGGTGTGTGGAGCGGTGTGGCGCACTGGCGCGCGGACTAGTATTGTGATGA 1156
QY 461 CCCCAACCCACTCTCCCTGCTGTAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGAT 520
DB 1157 CCCAGACTCCCACTCTCTGCTGTTTTCAGCAGGAGACAGGGTTTACCATAACCTGCAAGG 1216
QY 521 CTAGTCAGAGCCTTTTACACAGATTAATGGAATCACTATTACATTTGTGTACCTGCAGAGC 580
DB 1217 CCAGTCAGAG-----TGTGATTAATGATGTAGCTTGTGTACCAACAGAGC 1261
QY 581 CAGGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGGTCCAG 640
DB 1262 CAGGCGAGTCTCTACACTGCTATATCTCTATACATCCAGTCGCTAGCGTGGATCCCTG 1321
QY 641 ACAGGTTCACTGGCGAGTGGATCAGGACAGATTTCACTCAAGATCAGCAGAGTGGAG 700
DB 1322 ATCGCTTCATTGGCAGTGGATATGGGACGATTTCACTTTCCACATCAGCAGCTTTCAGG 1381
QY 701 CTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTACACGTTTCGGAG 760
DB 1382 CTGAGAGCTTGGCAGTTTATTTCTGTGTCAGCAAGTATTAATTTCTCTCCGACGTTCCGTG 1441
QY 761 GGGGACCAAGCTGGAATAAAGAA 786
DB 1442 GAGGACCAAGCTGGAATAAATAA 1467

RESULT 15
US-10-060-585-1
; Sequence 1, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DYO023.001CP1
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB 9714230.1
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 729
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 514 ScFv
US-10-060-585-1
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Query Match 38.0%; Score 315.4; DB 9; Length 729;
Best Local Similarity 67.9%; Pred. No. 3.4e-91;
Matches 503; Conservative 1; Mismatches 198; Indels 39; Gaps 3;
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QY 67 GCGGTTCAACTCGACGAGTCTGGGCTGAGCTGGTGAGCCTGGGGCTTCAGTGAGCGTG 126
DB 1 GAGGTCACAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
QY 127 TCTGCAAGCCTTCGGGCTACACATTTACTGACTATGAAATACACTGGGTGAGGAGACA 186
DB 61 TCTGCAAGCCTTCGGTACTTACTTACTGCTGCTACTACATGCTGGGTGAAGAGAGC 120
QY 187 CTTGTGCATGGCTGGAATGGATTGGAGCTATTGATCTGAAACTGGTGGTACTGCTTAC 246
DB 121 CATGGAAGAGAGCTTGAGTGGATTGGACGTAATTAATCTCAATGAGTGTACTCTCTAC 180
QY 247 AATCAGAAGTTCAAGGACAGAGCCATAGTACTGTAGACAAATCTCCAGCACAGCCTAC 306
DB 181 AACCAGAAATTCAGGACAGAGGCCATATTAACTGTAGACAAGTCAATCCACCAGCCTAC 240
QY 307 ATGGAGCTCCGAGCCTGACATCTGAAGACTCTGCCGTCTATTACTATATAAAGAT---- 361
DB 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGTCTATTACTGTGCAAGATCTACT 300
QY 362 -----GGTTTGAGGACTGGGCGCAAGGAGCTCTGGTCACTGTCTCTGCA 405
DB 301 ATGATTACGAACATAATGTTATGGACTACTGGGTCAAGTAACCTCAGTCACCGCTCTCTCA 360
QY 406 GAGGTTAAATCTCAGGACTCTGGCTCCGAATCCAAACCCGGG---ATGTTGTGATGACC 462
DB 361 GGTGTGTGGAGCGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATGACC 420
QY 463 CCAAAACCACTCTCCCTGCTGCTGCTGATCTTGGAGATCAAGCCTCCATCTCTTGCAGATCT 522
DB 421 CAGACTCCCAACATCTCTGCTGCTTTTCAGCAGGAGACAGAGGTTTACCATAACCTGCAAGCC 480
QY 523 AGTCAGAGCCTTTTACACAGTAATGGAATCACTATTATTACATTTGGTACTCTGAGAGCCA 582
DB 481 AGTCAGAG-----TGTGATTAATGATGTAGDTTGGTATCCCAACAGAGCCA 525
QY 583 GGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGTCCTCCAGAC 642
DB 526 GGGCAGTCTCTACACTGCTCATATCCTATACATCAAGTCGCTACGCTGGAGTCCCTGAT 585
QY 643 AGGTTTCAGTGGCAGTGGATCAGGAGACAGATTTTACACTCAAGATCAGCAGAGTGGAGGCT 702
DB 586 CGCTTCATTGGCAGTGGATATGGAGCGGATTTCACTTTCAACCATCAGCACTTTGAGGCT 645
QY 703 GAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTACACGTTGGAGGG 762
DB 646 GAAAGACCTGGCAGTTTATTTCTGTGCAAGAAATTAATTTCTCTCCGACGTTCCGTGGA 705
QY 763 GGCACCAAGCTGGAATAAATA 783
DB 706 GGCACCAAGCTGGAATAAATA 726
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Job time : 117 secs
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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 23:07:58 ; Search time 38 Seconds  
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Title: US-09-358-321C-31  
Perfect score: 830  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15333831 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	407.6	49.1	749	4	US-08-983-035A-46
2	405.2	48.8	1611	4	US-08-983-035A-37
3	380.4	45.8	772	1	US-08-331-398A-33
4	380.4	45.8	772	2	US-08-331-397B-33
5	380.4	45.8	772	2	US-08-759-804A-33
6	380.4	45.8	772	4	US-09-227-693-33
7	362.4	43.7	864	4	US-09-423-439-47
8	349	42.0	741	4	US-09-227-693-31
9	348.2	42.0	738	1	US-08-331-398A-31
10	348.2	42.0	738	2	US-08-331-397B-31
11	348.2	42.0	738	2	US-08-759-804A-31
12	347.4	41.9	2010	3	US-09-070-637-19
13	338.8	40.8	814	2	US-08-752-844-65
14	338.2	40.7	2019	4	US-09-423-439-31
15	338.2	40.7	2025	4	US-09-423-439-37
16	337.2	40.6	831	2	US-08-403-853-17
17	332.6	40.1	1095	3	US-08-875-811-52
18	332.6	40.1	1098	3	US-08-875-811-54
19	327.6	39.5	965	1	US-08-388-672A-22
20	327.6	39.5	965	3	US-09-080-554-22
21	326.4	39.3	891	2	US-08-894-922A-9
22	321.8	38.8	907	3	US-09-184-658-9
23	321	38.7	797	2	US-08-894-922A-13
24	320.4	38.6	384	1	US-08-482-882-44
25	320.4	38.6	384	1	US-08-483-389-44
26	320.4	38.6	384	2	US-08-487-113D-44
27	320.4	38.6	384	2	US-08-473-503-44

Sequence 44, Appl

Sequence 44, Appl  
Sequence 44, Appl  
Sequence 44, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 6, Appl  
Sequence 8, Appl  
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Sequence 7, Appl  
Sequence 6, Appl  
Sequence 7, Appl  
Sequence 10, Appl  
Sequence 8, Appl  
Sequence 18, Appl  
Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-08-983-035A-46  
; Sequence 46, Application US/08983035A  
; Patent No. 6326464  
; GENERAL INFORMATION:  
; APPLICANT: CONSEILLER, EMMANUEL  
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FINNegan, Henderson, Farabow, Garrett &  
; DUNNER, LLP  
; STREET: 1300 I Street, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/983,035A  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR96/01111  
; FILING DATE: 17-JUL-1996  
; APPLICATION NUMBER: FR 95/08729  
; FILING DATE: 19-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Strauss, William L.  
; REGISTRATION NUMBER: 47,114  
; REFERENCE/DOCKET NUMBER: 03804.0142  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4400  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 749 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Query Match 49.1% Score 407.6; DB 4; Length 749;

Best Local Similarity 74.1%; Pred. No. 2.1e-114;  
Matches 547; Conservative 0; Mismatches 179; Indels 12; Gaps 2;

QY 58 GCCTTTGGGGGGTTCAATCGCAGCAGTCTGGGGCTGAGCTGGTGGAGCCTGGGGCTTCA 117  
Db 1 GCCATGGCCAGGTGCGAGTGCAGAGTCAGGGCGAGCTTGTGGGTGAGGGCCCTCA 60

QY 118 GTGAGCTGTCTCCAAAGGCTTGGGGCTACACATTTACTGACTATGAATAACACTGGGTG 177  
Db 61 GTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAGAGACTACTATATGCACCTGGTG 120

QY 178 AGGCAGACACTGTGCATGGCTGGATGGATGGAGCTATTGATCTGAACTGGTGGT 237  
Db 121 AAGCAGAGGCTGAACAGGCGCTGGAGTGGATGGATGGATGGATGGATGGATGGAT 180

QY 238 ACTGCTCAATCAGAAAGTTCAAGGACAAGGCCATAGTACTGTAGACAAATCTCCAGC 297  
Db 181 ACTGAATATGCCCGAAGTTCAGGCAAGGCCACTATGACTGCAGACACATCTCCAAT 240

QY 298 ACAGCTACATGAGCTCGGAGCTGACATCTGAACTCTGAACTCTGCGCTCTATTATACA 357  
Db 241 ACAGCTACCTGACCTCAGCAGCTCGCATCTGAGACACTGCGCTCTATTATGTAAT 300

QY 358 AGAT-----GGTTTGAGGACTGGGGCCCAAGGACTCTGGTCACTGTCTGCGAG 408  
Db 301 TTTTACGGGAGTCTTTGGACTACTGGGGCCCAAGGACACCGGTACCGTCTCCTCAGGT 360

QY 409 GGTAAATCTCTCA---GGATCTGGCTCCGAATCCAAACCCGGGGATGTTGTGATGACCCCA 465  
Db 361 GGAGCGGTTTCAGCGGAGGTGGCTCTGGCGGTGCGGATCGGATGTTTGTGACCCAA 420

QY 466 AACCACTCTCCCTGCTGCTGAGCTTGGAGATCAAGCTCCATCTCTTGCAGATCTAGT 525  
Db 421 ACTCACTCACTTTGTGCGTTTACCAATTTGGCAACACCGCTCCATCTCTTCAAGTCAAGT 480

QY 526 CAGAGCTCTTTACACAGTAATGGAATCACTTATTTATGTTGGTACCTGCAGAGCCAGGC 585  
Db 481 CAGAGCTCTTGGATGATGATGGAAGACATATTTGATTTGGTTTACAGAGCCAGGC 540

QY 586 CAGTCTCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGGTCCCAAGCAGG 645  
Db 541 CAGTCTCAAAGCGCTTAATCTATCTGTTGTCTAAACCTGGACTCTGGAGTCCCTGACAGG 600

QY 646 TTCAGTGGCAGTGATCAGGACAGATTTACACTCAAGATCAGCAGAGTGGAGCTGAG 705  
Db 601 TTCAGTGGCAGTGATCAGGACAGATTTACACTGAAATCAACAGAGTGGAGCTGAG 660

QY 706 GATCTGGAGTTTATTTCTCTCTCAAGTACACATGTTCCGTACAGCTTCCGAGGGGG 765  
Db 661 GATTGGAGTTTATTTCTGTCGAAGGTACACATTTCTCCGTCACTGTTGCGTGGG 720

QY 766 ACCAAGCTGGAATAAA 783  
Db 721 ACCAAGCTGAGCTGAAA 738

RESULT 2

US-08-983-035A-37

; Sequence 37, Application US/08983035A

; Patent No. 6326464

; GENERAL INFORMATION:

; APPLICANT: CONSEILLER, EMMANUEL

; BRACCO, LAURENT

; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FINNIGAN, HENDERSON, FARABOW, GARRETT &

; DUNNER, LLP

; STREET: 1300 I Street, NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT NUMBER: US/08/983,035A  
FILING DATE: 20-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICANT NUMBER: PCT/FR96/01111  
FILING DATE: 17-JUL-1996  
APPLICANT NUMBER: FR 95/08729  
FILING DATE: 19-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Strauss, William L.  
REGISTRATION NUMBER: 47,114  
REFERENCE/DOCKET NUMBER: 03804.0142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1611 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1605  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-08-983-035A-37

Query Match 48.8%; Score 405.2; DB 4; Length 1611;  
Best Local Similarity 74.1%; Pred. No. 1.6e-113;  
Matches 544; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

QY 62 TTGCGGCGGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGGAGCGCTGGGGCTTCAAGTGA 121  
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QY 122 CGCTGTCCTGCAAGGCTTCGGGCTACACATTTACTGACTATGAAATACACTGGGTGAGC 181  
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QY 182 AGACACCTGTGATGGCTGGATGGATGGAGCTATTGATCTGAAACTGGTGGTACTG 241  
Db 122 AGAGGCTTCAACAGGCGCTGGAGTGGATGGATTTGATCTGAGAAATGGGTGATCTG 181

QY 242 CCTACAATCAGAAAGTTCAAGGACAAGGCCATAGTACTGTAGACAAATCTCCAGCACAG 301  
Db 182 AATATGCCCGAAGTTCAGGGGAGGCCACTATGACTGCAGACACATCTCTCAATACAG 241

QY 302 CCTACATGAGCTCCGCGAGCTGACATCTGAAGACTCTCCCGTCTATTACTATACAAGAT 361  
Db 242 CCTACCTGAGCTCAGCAGCTGGCATCTGAGGACACTGCCGTCTATTATTGTAATTTT 301

QY 362 -----GGTTTGAGGACTGGGGCCAGGAGCTCTGGTCACTGTCTCTGCGAGAGGTA 412  
Db 302 ACGGGGATGCTTTGGAGTACTTGGGGCCAAAGGACACCGGTCTCTCCAGTGGAG 361

QY 413 AATCTCTCA---GGATCTGGCTCCGAATCCAAACCCGGGGATGTGTGATGACCCCAACC 469  
Db 362 GCGGTTTCAGGCGGAGGTGGCTCTGGGGTGGCGGATCGGATGTTTGTAGACCCAACTC 421

QY 470 CACTCTCCCTGCTGCTGAGTCTTTGGAGATCAAGCCTCCATCTCTTTCAGAGATCTAGTCAGA 529  
Db 422 CACTCACTTTGTGCGTTTACCAATTGGACAACAGCCTCCATCTCTTTCGAAGTCAAGTCAGA 481

QY 530 GCCTTTTACACAGTAAATGGAATCAGCTATTATTTACATTTGGTACCTGCAGAGCCAGCCAGT 589







FILING DATE: 12-OCT-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weber, Ellen L.  
 REGISTRATION NUMBER: 32,762  
 REFERENCE/DOCKET NUMBER: 015280-12614005  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 33:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 772 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 FEATURE:  
 NAME/KEY: -  
 LOCATION: 1..772  
 OTHER INFORMATION: /note= "single-chain antibody fusion  
 OTHER INFORMATION: protein of B1 monoclonal antibody  
 OTHER INFORMATION: Variable Heavy chain (V-H) and Variable  
 OTHER INFORMATION: Light chain (V-L) Fv region joined by a  
 OTHER INFORMATION: (Gly-4Ser)-3 peptide linker"  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 27..770  
 US-08-759-804A-33

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? NUCLEIC ACID:
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
? FEATURE:
?   NAME/KEY: -
?   LOCATION: 1..772
?   OTHER INFORMATION: /note= "single-chain antibody fusion
?   OTHER INFORMATION: protein of B3 monoclonal antibody
?   OTHER INFORMATION: Variable Heavy chain (V-H) and Variable
?   OTHER INFORMATION: Light chain (V-L) Fv region joined by a
?   OTHER INFORMATION: (Gly-4Ser)-3 peptide linker"
?   FEATURE:
?   NAME/KEY: CDS
?   LOCATION: 27..770
? US-08-759-804A-33

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	Query Match	45.8%;	Score 380.4;	DB 2;	Length 772;
	Best Local Similarity	72.0%;	Pred. No. 3.9e-106;		
	Matches 533;	Conservative 0;	Mismatches 186;	Indels 21;	Gaps
QY	66	GGCGGTTCAACTGCAGCAGTCTCGGGCTGAGCTGGGTGAGGCCTGGGGCTTCACTGACGCT	125		
DB	29	GGATGTGAAGCTGGTGAGTCTCGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCTGAAACT	88		
QY	126	GTCTTCGAAGGCTTCGGGCTACACATTTACTGACTATTGAATAACACTGGGTGAGGCAGAC	185		
DB	89	CTCTGTGCAACCTCTGGATTCACTTTCAGTGACTATTACATGTTNTGGTTCGCCAGAC	148		
QY	186	ACCTGTGCATGGCCTGGAATGGAGCTATTGATCTCTGAAACTGGTGGTATCTGCCTA	245		
DB	149	TCCAGAGAAGAGGCTGGAGTGGCTGCGATACATTAGTAATGATGATAGTTCCGCGCTTA	208		
QY	246	CANTCAGAAGTTCAAGGACAAGGCCATAGTGACTGTAGACAAATCTCCAGCACAGCCTA	305		
DB	209	TTCAGACACTGTAAAGGGCCGTTCCACCATCTCCAGAGACAATGCCAGGAACACCCCTCTA	268		
QY	306	CATGGAGCTCCGACGCTGCATCTCGAAGACTCTGCGGCTCTATTACTATACAAGA----	360		
DB	269	CTTGCAATGAGCCGCTGAAGTCTGAGGACACAGCCATATATCTGTGCAGAGGACT	328		
QY	361	-----TGTTTTGAGACTGGGCCAAGGACTCTCGTCACTGTCTCTGCA--	405		
DB	329	GGCCTGGGAGACCTGGTTTTGCTTTACTGGGGCCAAGGACTCTCGTCACTGTCTCTCAG	388		
QY	406	-GAGGCTAAATCTCAGGATCTCGCTCCGNAATCCAAACCCGGGGATGTTGTGATGACCC	464		
DB	389	CGAGGCGGATCCGGTGGTGGCGGATCTGGAGTGGCGGAAGCGATGTGCTGATGACCCA	448		
QY	465	AAACCCCACTCTCCCTGCTGTCACTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAG	524		
DB	449	GTCTCCATTGAGTTTACCTGTCACTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAG	508		
QY	525	TCAGAGCCTTTTACACAGTAATGGAATACCTATTTACATTTGATCCTGCAGAGCCAGG	584		
DB	509	TCAGATCATTTGATAGTAATGGAACACCTTTTAGAATGTACTCTGCAGAAACCCAGG	568		

QY	585	CCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTTCCTGGGTCCACACAG	644
Db	569	CCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTTCCTGGGTCCACACAG	628
QY	645	GTTTCAGTGGCAGTGGATCAGGGACAGATTTACACTCAAGATCAGCAGAGTGGAGGCTGA	704

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Db 29 GGATGCAAGCTGGTGGAGTCTGGGGAGGCTTAGTCAGCCTGGAGGTCCTGAAACT 88
QY 126 GTCTGCAAGGCTTCGGGTACACATTACTGACTATGAATACACTGGGTGAGGAGAC 185
Db 89 CTCTGTGCAACTCTGGATTACTTTCAGTGACTATTACATGATTGGGTTCGGCAGAC 148
QY 186 ACCTGTGCATGGCTGGAATGGAGTATTGATCTCTGAAACTGGTGTACTGCCTA 245
Db 149 TCCAGAGAAGAGCTGGAGTGGCTCGCATACATTAGTAATGATGATAGTTCCGCGCTTA 208
QY 246 CAATCAGAAGTTCAAGACAAGGCATAGTACTGTAGACAAATCTCCAGACACGCTA 305
Db 209 TTCAGACACTGTAAGGGCGGTTCACCATCTCCAGAGACAATGCCAGGAACACCTCTA 268
QY 306 CATGGAGCTCCGAGCTGACATCTGAAGACTCTGCGCTATTACTATACAGA----- 360
Db 269 CTGCAATGAGCGCTGAGTCTGAGGACAGCCATATATCTGTGCAAGAGACT 328
QY 361 -----TGGTTTGGAGCTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA-- 405
Db 329 GGCTGGGAGCGCTGTTTCTTACTGGGCGCAAGGACTCTGGTCACTGTCTCTCAGG 388
QY 406 -GAGGTAAATCTCAGGACTCTGGCTCCGAATCCAAACCGGGATGTTGTGATGACCCC 464
Db 389 CGAGGCGGATCCGGTGGTGGCGGATCTGGAGGTGGCGGAAGGATGTGCTGATGACCCA 448
QY 465 AAACCCACTCTCCCTGCTCTGCTGAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAG 524
Db 449 GTCTCAATGAGTTTACTCTGAGTCTTGGAGATCAAGCCTCCATCTCTTGGAGATCTAG 508
QY 525 TCAGAGCTTTTACACAGTAATGGAATCACTATTACATTTGATGCTGACAGAGCCAGG 584
Db 509 TCAGATCAITGTACATAGTAATGGAACACCTATTAGATGTACTCTGCAGAAACAGG 568
QY 585 CGAGTCTCMAAGCTCTGATCTACAAAGTTTCCAAACCGATTCTTGGGGTCCAGACAG 644
Db 569 CCAGTCTCMAAGCTCTGATCTACAAAGTTTCCAAACCGATTCTTGGGGTCCAGACAG 628
QY 645 GTTCAGTGGGAGTGGATCAGGAGACAGATTTACACTCAAGATCAGACAGAGTGGAGGCTGA 704
Db 629 GTTCAGTGGGAGTGGATCAGGAGACAGATTTACACTCAAGATCAGACAGAGTGGAGGCTGA 688
QY 705 GGATCTGGGAGTTATTCTGCTCTCAAAAGTACACATGTTCCGTACACAGTTCGGAGGGG 764
Db 689 GGATCTGGGAGTTATTACTGCTTTCAAGGTTCAACATGTTCCATTCAAGTTCGGCTCGG 748
QY 765 GACCAAGCTGGAATAAAG 784
Db 749 GACAAAGCTGGAATAAAG 768
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## RESULT 7

IS-09-423-439-47

Sequence 47, Application US/09423439

Patent No. 6339070

## GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles

BLAKEY, David Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NO. 6339070-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-423-439-47
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Query Match 43.7%; Score 362.4; DB 4; Length 864;
Best Local Similarity 70.6%; Pred. No. 1.2e-100;
Matches 569; Conservative 0; Mismatches 201; Indels 36; Gaps 5;

QY 46 GCGGGCGATTCTGCCCTTTGGCGCGGTTCAACTGCGAGCAGTCTGGGGCTGAGCTGTGAGG 105
Db 46 GCTGCCCAACACGAGCTGGCCAGGTCCAACTGCGAGCAGCTGGGGCTGAACCTGGTGAAG 105
QY 106 CTTGGGGTTCAGTGACACCTGTCTGCAAGGCTTCGGGCTACACATTTACTACTATGAA 165
Db 106 CTTGGGGTTCAGTGACAGCTGTCTGCAAGGCTTCGGCTACACCTTCACCGGCTACTGG 165
QY 166 ATACACTGGGTGAGGCGACACCTGTGCTGATGGCTTGGAAATGGATTGGAGCTATTGATCT 225
Db 166 ATACACTGGGTGAGGCGAGGCTGTGCAAGGCTTGGTGGATTGGAGGCTTAATCTCT 225
QY 226 GAAACTGTGTGTTACTGCTTACAATCAGAAAGTTTCAAGGACAAGGCCATAGTACTGTAGAC 285
Db 226 AGTACCGGTCTGTTGACTTACAATGAGAAGTTTCAAGGACAAGGCCACACTGACTGTAGAC 285
QY 286 AATCTCTCCAGCAGACGCTACATGGAGCTCCGCGCGCTGACATCTGAAGACTCTGCCGTC 345
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QY 346 TATTACTATACAAGATGG-----TTTGAGGACTTGGGGCCAA 381
Db 346 TATTACTTGAAGAGAGAGGCGCTATGTTACGACGATGCTATGACTACTTGGGGCCAA 405
QY 382 GGGACTCTGGTCACTGTCTCTGCA---GAGGGTAAATCTCAGGATCTGGTTCGGAATCC 438
Db 406 GGGACACCGTTCACCGTCTCTCAGGTGGCGGTGGCTGGGGCGGTGGTGGGTGGGTGGC 465
QY 439 AAACCCGGGAGTGTGATGACCCCAACCCACTCTCCCTGCCCTGTCAGTCTTGGAGAT 498
Db 466 GCGGATCTGACATTGAGCTCTCAGTCTCCATCTCCCTGGGCTGTGTACAGCAGAGAG 525
QY 499 CAAGCCTCCATCTCTTGCAGATCTAGTACAGACCTTTTACACAGTAATG---GAATCACC 555
Db 526 AAGGTACCATGAGTGCATTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 585
QY 586 TATTACATTTGGTACCTCCAGAGCCAGGCGAGTCTCCAAAGCTCTGATCTTACAAAGTT 615
Db 586 TACTTGGCTTGGTACACAGCAGACGAGGCGAGTCTCTAAAGTCTGATCTTATTTGGGCA 645
QY 616 TCCAAACGATTTCTGGGGTCCAGACAGGTTTCAAGTGGAGTTCAGTGGAGTTCAGGACAGATTC 675
Db 646 TCCACTAGGACATCTGGGGTCCCTGATCGCTTTCAGGCGAGTGGATCTGGGACAGATTC 705
QY 676 ACACCTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAAGT 735
Db 706 ACTCTCACCATCAGCAGTGTGAGGCTGAAGACCTGGCAATTTATTACTGCAAGCAATCT 765
QY 736 ACACATGTTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAA---GAAGAAAAA 792
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Db 766 TATACTCTTCGG---ACGTTCCGTTGGAGGACCAAGCTCGAGATCAAAACGGGAACAAAA 822

Qy 793 CTCATCTCAGAAGAGGATCTGAATTA 818  
Db 823 CTCATCTCAGAAGAAGATCTGAATCA 848

## RESULT 8

US-09-227-693-31  
; Sequence 31, Application US/09227693  
; Patent No. 6287562  
; GENERAL INFORMATION:  
; APPLICANT: PASTAN, Ira  
; APPLICANT: BENHAR, Itai  
; APPLICANT: PADLAN, Eduardo A.  
; APPLICANT: JUNG, Sun-Hee  
; APPLICANT: LEE, Byungkook  
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY  
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Stewart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/227,693  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/331,396  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 15280-126-1-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 741 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1..741  
; OTHER INFORMATION: /note= "Sequence encoding humanized  
; Patent No. 6287562  
; OTHER INFORMATION: B3 (Fv)"

US-09-227-693-31  
Query Match 42.0%; Score 349; DB 4; Length 741;  
Best Local Similarity 69.4%; Pred. No. 1.4e-96;  
Matches 513; Conservative 0; Mismatches 205; Indels 21; Gaps 2;

Qy 66 GCGCGTTCACTGCAGCAGTCTGGGCTGAGCTGGTGGAGGCTGGGCTTCAGTGACGCT 125  
Db 3 GCGATGTGAAGCTGGTGGAGTCTGGGGGAGGCGCTGCTGACGCGCGGCTCCCTGAAACT 62

Qy 126 GTCTGTCAAGCTTCGGGCTACACATTTACTGACTATGAAATACACTGGGTGAGGCAGAC 185  
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Qy 186 ACCTGTGCATGGCCTGGAATGGAGTTCGAGCTATTGATCCCTGAAACTGGTGTACTGCCTA 245  
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Qy 246 CAATCAGAAGTTCAAGSACAAGGCCCATAGTACTGTAGACAAAATCCTCCAGCACAGCCTA 305  
Db 183 TTCAGACACTGTAAAGGCGGTTTACCATCTCTAGAGACAAATAGCAAGAACACACCTCTA 242  
Qy 306 CATGGAGCTCCGAGCCTGACATCTGAAGACTCTGCGGTCTATTACTATATACAAGA----- 360  
Db 243 CTGCAAAATGAACGCTGCGCGCCGAGGACACAGCCATATATTCCTGTGCAAGAGGACT 302  
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Db 303 GGCTGGGAGCCTGGTTTCTTACTGGGSCCAAGGACTCTGCTACTCTCTCTCTCTCAGG 362  
Qy 406 -GAGGTTAAATCTCAGGATCTGGCTCCGAATCCAAACCCGGGATGTTGTGATGACCCC 464  
Db 363 CGGAGGCGGATCCGGTGGTGGCGGATCTGGAGGTGGCGGAAGCGATGCTGTGATGACCCA 422  
Qy 465 AAACCCACTCTCCCTGCTCTCAGTCTTTGGAGATCAAGCCTCCATCTCTTCGAGATCTAG 524  
Db 423 GTCTCCATTGAGTTTACTCTGTCACCCCGGAGAGCGGCGCTCCATCTCTTCGAGATCTAG 482  
Qy 525 TCAGAGCCTTTACACAGTAATGGAATCACCATTATTTACATTGGTACCTGCAGAGCCAGG 584  
Db 483 TCAGATCATTTGATAGTAATGGAACACCTATTTAGAAATGGTACCTGCAGAAACAGG 542  
Qy 585 CCAGTCTCAAAGCTCCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGTCCAGACAG 644  
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Qy 645 GTTCAGTGGCAGTGGATCAGGAGACAGATTTACACTCAAGATCAGCAGAGTGGAGGCTGA 704  
Db 603 GTTCAGTGGCAGTGGATCAGGAGACAGATTTACACTCAAGATCAGCAGAGTGGAGGCTGA 662  
Qy 705 GGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTTACACGTTTCGGAGGGG 764  
Db 663 GGACGTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCAGGTTCCATGTTCCATTCGCGCAGG 722  
Qy 765 GACCAAGCTGCAAAATAAAA 783  
Db 723 TACCAAGTCAAAATAAAA 741

## RESULT 9

US-08-331-398A-31  
; Sequence 31, Application US/08331398A  
; Patent No. 5608039  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark  
; APPLICANT: FitzGerald, David  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Pal, Lee  
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
; TITLE OF INVENTION: and Their Uses (as amended)  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,398A  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..738  
OTHER INFORMATION: /note= "Humanized B3 single-chain Fv"  
US-08-331-398A-31

Query Match 42.0%; Score 348.2; DB 1; Length 738;  
Best Local Similarity 69.5%; Pred. No. 2.4e-96;  
Matches 511; Conservative 0; Mismatches 203; Indels 21; Gaps 2;  
IQY 70 GTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGGAGGCTGGGGCTTCAGTGACGCTGTCC 129  
DB 4 GTGAAGCTGTGGAGTCTGGGGAGGGCTGTGCAGCCGGGGCTCCCTGAAACTCTCC 63  
IQY 130 TGCNAGGCTTCGGGCTACATTTACTGACTATCAATACACTGGGTGAGGCACACCT 189  
DB 64 TGTCAACCTCTGGATCTTTTCAGTGACTATTACATGATTGGGTTCGCCAGGCCCG 123  
IQY 190 GTGCATGGCTTGAATGGATTGGAGCTATTGATCCTGAAACTGGTGGTACTGCTCAAT 249  
DB 124 GGCAAGGCTTGGAGTGGTGGCGATACATTAGTATGATAGTTCGGCGCTTATCA 183  
IQY 250 CAGAAGTTCAAGGACAAAGGCATAGTACTGTAGACAAATCCTCCAGCAGGCTCATG 309  
DB 184 GACACTGTAAGGCGCGGTTCCACCATCTCTAGACAAATAGCAAGAACACCCCTCTACCTG 243  
IQY 310 GAGCTCCGCGACCTGACATCTGAGACTCTGGCTCTTACTATATACAAGA----- 360  
DB 244 CAATGAACCTGTGCGCGCGAGGACACAGCCATATTCCTGTGCAAGAGGACTGGCC 303  
IQY 361 -----TGGTTGAGGACTGGGGCAAGGAGCTGTGCTACTGTCTGCA---GAG 408  
DB 304 TGGGGAGCTGGTTGCTTACTGGGGCAAGGAGCTGTGCTACTGTCTCTCAGCGGA 363  
IQY 409 GGTAAATCTCAGGATCTGGCTCGGAATCCAAACCCGGGATGTTGTGATGACCCCAAC 468  
DB 364 GCGGATCCGGTGTGGCGCATCTGGAGGTGGCGGAAGCATGTGCTGATGACCCAGTCT 423  
IQY 469 CCACTCTCCCTGCTGTGCTGTGGAGATCAAGCTCCATCTCTTCAGATCTAGTCAG 528  
DB 424 CCATTGATTTACCTGTGACCCCGGGAGAGCCGGCTCCCATCTCTTCAGATCTAGTCAG 483  
IQY 529 AGCCTTTTACACAGTAATGGAATCACCTATTATACATTGGTACTGCAAGAGCCAGGCCAG 588  
DB 484 ATCATTTGACATAGTAATGNAACACCTATTAGATGTTGATCTGCAAGAACCCAGGCCAG 543  
IQY 589 TCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGGATTTTCTGGGGTCCCGACAGAGTTC 648

DB 544 TCTCCACAGCTGCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGTCCAGACAGGTTCC 603  
QY 649 AGTGGCAGTGGATCAGGACAGATTTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGAT 708  
DB 604 AGTGGCAGTGGATCAGGACAGATTTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGAC 663  
QY 709 CTGGGAGTTTATTTCTGCTCTCAAAAGTACACATGTTCCGTACACGTTTCGAGAGGGGACC 768  
DB 664 GTCCGAGTTTATTTACTGCTTTCAAGGTTTCAATGTTCCATTCAGTTTCGCCAGGGTACC 723  
QY 769 AAGCTGGAATAAAA 783  
DB 724 AAGTCAAAATAAA 738  
RESULT 10  
US-08-331-397B-31  
Sequence 31, Application US/08331397B  
Patent No. 5981726  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
Specific Antibody Fragments, Fusion Proteins, and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,397B  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126120US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..738  
OTHER INFORMATION: /note= "Humanized B3 single-chain Fv"  
US-08-331-397B-31

Query Match 42.0%; Score 348.2; DB 2; Length 738;  
Best Local Similarity 69.5%; Pred. No. 2.4e-96;  
Matches 511; Conservative 0; Mismatches 203; Indels 21; Gaps 2;



QY 529 AGCTTTTACACAGTAATGAATCACCTATTATTTACATTGGTACCTGCAGAACCCAGGCCAG 588  
Db 484 ATCAATTGACATAGTAATGGAACACACCTATTAGAAATGGTACCTGCAGAAACCCAGGCCAG 543  
QY 589 TCTCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTCTTCTGGGGTCCACAGACAGGTTT 648  
Db 544 TCTCCACAGCTGCTGATCTACAAAGTTTCCAAACCGATTCTTCTGGGGTCCACAGACAGGTTT 603  
QY 649 AGTGGCAGTGGATCAGGACAGATTTTCCAACTCAAGATCAGCAGAGTGGAGGCTTGAGGAT 708  
Db 604 AGTGGCAGTGGATCAGGACAGATTTTCCAACTCAAGATCAGCAGAGTGGAGGCTTGAGGAT 663  
QY 709 CTGGAGGTTTATTTCTGCTCTCAAGTACACATGTTCCGTTACAGTTCGAGGGGGGACC 768  
Db 664 GTCCGAGTTTATTTACTGCTTTCAAGGTTTCAATGTTCCATTTACGTTTCGGCCAGGGTACC 723  
QY 769 AAGCTGGAATAAAAA 783  
Db 724 AAGTGCNAATTAAA 738

RESULT 12  
US-09-070-637-19  
; Sequence 19, Application US/09070637A  
; Patent No. 6132722  
; GENERAL INFORMATION:  
; APPLICANT: SIEMENS, NATHAN O.  
; APPLICANT: YARNOLD, SUSAN  
; APPLICANT: SENTER, PETER D.  
; TITLE OF INVENTION: RECOMBINANT ANTIBODY-ENZYME FUSION PROTEINS  
; FILE REFERENCE: 9197F-83-1  
; CURRENT APPLICATION NUMBER: US/09/070, 637A  
; CURRENT FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: 60/045,888  
; EARLIER FILING DATE: 1997-05-07  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 2010  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: sequence for L49-sfv-bL including PeIB leader.  
US-09-070-637-19

Query Match 41.9%; Score 347.4; DB 3; Length 2010;  
Best Local Similarity 69.3%; Pred. No. 6,6e-96;  
Matches 534; Conservative 0; Mismatches 201; Indels 36; Gaps 3;

QY 46 GCGGCGCATTCCTCGCTTGGCGGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGAGG 105  
Db 137 GCTGCCACGCGCGGATGGCGAGGTGCAGCTTCAGAGTTCAGGACCTAGCCTCGTGAA 196  
QY 106 CTGGGGCTTCAGTGAAGCTGCTCTGCAAGGCTTCGGGTACACATTTACTGACTATGAA 165  
Db 197 CCTTCTCAGACTCTGCTCCCTCACTGTTCTGTCACTGGGACTCCATCACCAGTGGTTAC 256  
QY 166 ATACACTGGGTGAGGACAGCACCTGTGTCATGGCTCGAATGGATTGGAGCTATTGATCT 225  
Db 257 TGGAACTGATCCGGAAGTTCACAGGAATAAACTTGAATATATGGTTTACATAGC--- 313  
QY 226 GAACTGGTGGTACTGCTACATCAATCAAGAGTTTCAAGGACCAAGCCATAGTACTGTAGAC 285  
Db 314 GACAGTGGTATCACTTACTACTAATCCATCTCTCAAAAGTCGCAATTTCCATCACTCGAGAC 373  
QY 286 AATCTTCAGACAGCCTACATGGAGTCCGAGCCTCGACATCTGAAAGCTCTGCCGTC 345  
Db 374 ACATCCAAGAACCAATACTACTCTCCAGTTGAATTTTGTGACTGCTGAGGACACAGCCACA 433  
QY 346 TATTACTATACAGATGG-----TTTGAGGACTGGGGCCNAGG 384

Db 434 TATAACTGTGCAAGAGGACTCTGGCTACTTACTATGCTATGGACTACTGGGGTCAAGGA 493  
QY 385 ACTCTGTCCTCTCTCTGAGAGGGTAAATCT-----CAGGATCTGGCTCC 432  
Db 494 ACCTCTGTACCGTCTCTCTCAGGCTCGAGCTCGGGCTCTGGCAACCGGGCTCTGGCGAA 553  
QY 433 GAATCAAACCCGGGATGTTGTGATGACCCCAACCCACTCTCTCTGCTGTGAGTCTTT 492  
Db 554 GGCTCTACCAAGGGCGATTGTTGATGACCCAAACTCCAATCTCTCTGCTGTGAGTCTTT 613  
QY 493 GGAGATCAAGCCTCAATCTCTGAGATCTAGTACAGCCCTTTTACACAGTAATGAATC 552  
Db 614 GGAGATCAAGCCTCAATCTCTGAGGCTTAGTACAGAGCTCTTACACAGTAATGAATC 673  
QY 553 ACCTATTTACATTGTTACCTGAGAGGCGAGGCTCTCCAAAGCTCTGATCTTACAAA 612  
Db 674 ACCTATTTACATTGTTACCTGAGAGGCGAGGCTCTCCAAAGCTCTGATCTACAGA 733  
QY 613 GTTTCACACCGATTCTTCTGGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGAT 672  
Db 734 GTTTCACACCGATTCTTCTGGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGAT 793  
QY 673 TTCACACTCAAGATCAGCAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAA 732  
Db 794 TTCACACTCAAGATCAGCAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAA 853  
QY 733 AGTACACATGTTCCGTTACACAGTTCGGAGGGGGGACCAAGCTCGAAATAAAA 783  
Db 854 AGTACACATGTTCTCCGAGCTTCGGTGGAGGACCAAGCTGGAAATCAA 904

RESULT 13  
US-08-752-844-65  
; Sequence 65, Application US/08752844  
; Patent No. 5935821  
; GENERAL INFORMATION:  
; APPLICANT: Chatterjee, Malaya  
; APPLICANT: Foon, Kenneth A.  
; APPLICANT: Chatterjee, Sunil K.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,844  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 30414-20002.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 814 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..801  
US-08-752-844-65

Query Match 40.8%; Score 338.8; DB 2; Length 814;  
Best Local Similarity 68.9%; Pred. No. 1.8e-93;  
Matches 517; Conservative 0; Mismatches 212; Indels 21; Gaps 3;  
QY 55 TCTGCTTTGGCGGTTCAACTGACAGAGTCTGGGCTGAGCTGAGGCTTGGGCT 114  
DB 58 TGTGCTCTCCAGGTCAGGTCAGGAGTCAAGGCTTTCTGGTGGCCCTCACAG 117  
QY 115 TCAGTGAGCTCTCTCGAAGGCTTCGGCTACACATTTACTGACTAGTAATACATGG 174  
DB 118 AGCTGTCCATCAGATGACTGCTCGAGGTTCTCATTAACCACTATGTTGAAGCTG 177  
QY 175 GTGAGGAGACACCTGTGCTGGCTTGAATGGATTTGAGCTATTGATCTCTGAAACTGGT 234  
DB 178 ATTGCCAGCTCTCAGGAAAGGCTCTGGAGTGGCTGGGAGCAATTTGGGTGA---CGGG 234  
QY 235 GGTACTGCTACAATCAGAAAGTTTCAAGGACAAAGGCCATAGTACTGTAGCAAAATCTCTCC 294  
DB 235 ACCACAAATATCATTCAGCTCTCATATCCAGACTGAGCATCAGCAAGGATAACTCCAAG 294  
QY 295 AGCAGAGCTACATGGAGCTCCGAGCTGACATCTGAAGACTCTGCGCTTATTACTAT 354  
DB 295 AGCCAAGTTTCTTAAACTGAAAGTCTGCAAACTGATGACACGCGCCAGCTACTGT 354  
QY 355 ACAAGATGG-----TTTGAGACTGGGCGCAAGGACTCTGGTCACTGTG 399  
DB 355 GCCAACTGGTAAGTACTAGGCTCTGAGCTACTTGGGTCAAGGAACTCATGTCACCGTC 414  
QY 400 TCTCAGAGGGTAAATCCTCAGGATCTGGCTCCGAATCCAAACCCGG---GGATGTTTG 456  
DB 415 TCCTCAGGGGAGTGGCTCGGGCGGTGGCGCTCGGTGGCGCGGATCCGATGTTTG 474  
QY 457 ATGACCCCAAAACCACTCTCCCTGCTGTAGTCTTGGAGATCAAGGCTTCACTCTTGC 516  
DB 475 ATGACCAAACTCCACTCTCCCTGCTGTAGTCTTGGAGATCAAGGCTTCACTCTTGC 534  
QY 517 AGATCTAGTCAGAGCTTTTACACAGTAATGGAATCACTTATTTACATTTGATCTCAG 576  
DB 535 AGATCTAGTCAGAGCTTTTACATAGTATGGAACCACTTATTTAGATGATGATCTACAG 594  
QY 577 AAGCAGGCGAGCTTCCAAAGCTCTCATCTACAAAGTTTCCAAACCGATTTCTTGGGCTC 636  
DB 595 AAACAGGCGAGCTTCCAAAGCTCTCATCTACTTTGTTTCCAAACCGATTTCTTGGGCTC 654  
QY 637 CCAGACAGGTTCAAGTGGAGTGGATCAGGACAGATTTACACTCAAGATCAGCAGAGTG 696  
DB 655 CCAGACAGGTTCAAGTGGAGTGGATCAGGACAGATTTACACTCAAGATCAGCAGAGTG 714  
QY 697 GAGGCTGAGGATCTGGAGTATTCTTCTGCTCTCAAAAGTACACATGTTCCGTACACGTT 756  
DB 715 GAGGCTGAGGATCTGGAGTATTCTTCTGCTCTCAAAAGTACACATGTTCCGTACACGTT 774  
QY 757 GGAGGGGGACCAAGCTGGAATAAAGAA 786  
DB 775 GGTGGAGGACCAAGCTGGAATAAAGAA 804

RESULT 14  
US-09-423-439-31  
Sequence 31, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
Zip: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423.439  
FILING DATE: 09-No. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2019 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-423-439-31

Query Match 40.7%; Score 338.2; DB 4; Length 2019;  
Best Local Similarity 70.3%; Pred. No. 4.1e-93;  
Matches 524; Conservative 0; Mismatches 188; Indels 33; Gaps 4;  
QY 69 GGTCAACTGACAGCTCTGGGCTGAGCTGGTGAAGCCCTGGGGCTTCACTGAGCTGTC 128  
DB 60 GGTCAACTGACAGCTCTGGGCTGAACTGGTGAAGCCCTGGGGCTTCACTGAGCTGTC 119  
QY 129 CTCAAGGCTTGGGCTAGACATTTACTGACTATGAATACACTGGGTGAGGAGACACC 188  
DB 120 CTCAAGGCTTCTGGCTAGACCTTCAACCGCTACTGCGCTACTGCGGTGAAGCAGAGGCC 179  
QY 189 TGTGATGCGCTGGAATGGATGGAGCTATTGATCTGAACTGGTGGTACTGCTACAA 248  
DB 180 TGGACAAGGCTTGAATGGATGGAGAGGTTAATCTAGTACCGGCTGTTCTGACTACAA 239  
QY 249 TCAGAAAGTTCAAGCAAGGCCATAGTACTGTAGACAAATCTCCAGCACAGCCTACAT 308  
DB 240 TGAGAAGTTCAAGCAAGGCCACACTGACTGTAGACAAATCTCCACACAGCCTACAT 299  
QY 309 GGAGCTCCGAGCTGACATCTGAAGACTCTGCGCTTATTACTATACAAGATGG----- 363  
DB 300 GCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTCAAGAGAGAGGCC 359  
QY 364 -----TTTCAAGGACTGGGGCCAAAGGACTCTGCTGCTCTCTCTGC 404  
DB 360 CTATGTTTACGAGATGCTTATGAGTACTGGGGCCAAAGGACCAACCGTCAACCGTCTCTC 419  
QY 405 A---GAGGGTAAATCTCTAGGATCTGGCTCCGAATCCAAACCCGGGGATGTTGTGTATGAC 461  
DB 420 AGGTGCGGTGGCTCGGGCGGTGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 479  
QY 462 CCCAAACCCACTCTCCCTGCTGCTGAGTCTTGGAGATCAAGCCTTCATCTCTTTGAGATC 521  
DB 480 ACAGTCTCCATCTCCCTGGCTGTGTGACAGGAGAGAGGTCACCATGAGCTGCAAAATC 539  
QY 522 TAGTCAGAGCTTTTACACAGTAA---TGAATCACTTATTTACATTGTTGTTGCTGAGAA 578  
DB 540 CAGTCAGAGTCTCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACAGCAGAG 599  
QY 579 GCAGGCCAGTCTCCAAAGCTCTGATCTTACAAAGTTTCCAAACCGATTTCTTGGGGTCCC 638  
DB 600 ACCAGGGCAGTCTCTTAAGTCTGATCTATTGGGCATCCATAGGACATCTGGGGTCCC 659



QY 639 AGACAGGTTCACTGGCAGTGGATCAGGACAGATTTCCAACTCAGATCAGAGAGTGGA 698  
Db 660 TGATCGCTTCCAGAGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGTGGA 719  
QY 699 GGCTGAGGATCTGGAGCTTTATTTCTCTCTCTCAAGTACACATGTTCCGTACACGTTGG 758  
Db 720 GGCTGAGACCTGGCAATTTATTTACTGCAAGCAATCTTATCTCTTCGG---ACGTTGG 776  
QY 759 AGGGGGACCAAGCTGGAATAAAA 783  
Db 777 TGGAGGCACCAAGCTCGAGATCAA 801

## RESULT 15

US-09-423-439-37

Sequence 37, Application US/09423439

Patent No. 6339070

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439

FILING DATE: 09-No. 6339070-1999

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-MAY-1997

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 2025 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

IS-09-423-439-37

Query Match 40.7%; Score 338.2; DB 4; Length 2025;  
Best Local Similarity 70.3%; Pred. No. 4,1e-93;  
Matches 524; Conservative 0; Mismatches 188; Indels 33; Gaps 4;  
Y 69 GGTCAACTGCAGCAGTCTGGGCTGAGCTGGTGGGCTGGGCTTTCAGTGACGCTGTC 128  
b 60 GGTCAACTGCAGCAGCCTGGGCTCAACTGGTGAAGCCTGGGCTTTCAGTGACGCTGTC 119  
Y 129 CTGCAAGGCTTCGGGCTACACATTTACTGACTATGAAATACACTGGGTGAGGCACACC 188  
b 120 CTGCAAGGCTTCGGGCTACACCTTACCAGGCTTCTGAGTACGCTGCTGCTGCTGCT 179  
Y 189 TGTGATGCGCTGGGCTGAGTGGAGCTTATGATCTCTGAACTGGTGGTACTGCTGCTGCT 248  
b 180 TGGACAGGCTTGTAGTGGATTTGGAGAGGTTAATCTAGTACCGGTCTGCTGCTGCTGCT 239  
Y 249 TCAGAAAGTTCAAGGACCAAGGCCATAGTACTGTAGCAAAATCTCCAGCACAGCCTACAT 308  
b 240 TGAGAAGTTCAAGAACCAAGGCCACACTGACTGTAGCAAAATCTCCACACAGCCTACAT 299

QY 309 GGAGTCCCCAGCCTGACATCTGAAGACTCTCCCGTCTATTACTATACAAAGATGG----- 363  
Db 300 GCAACTCAGCAGCCTGACATCTGAGGACTCTCGGCTCTATTACTGTGCAAGAGAGAGGCG 359  
QY 364 -----TTTGAGGACTGGGGCCCAAGGACTCTGGTCACTGTCTCTCG 404  
Db 360 CTATGTTTACGACGATGCTATGGACTTCTGGGGCCCAAGGACCAAGGCTCACCCTCTCTC 419  
QY 405 A---GAGGTAATCTCAGGATCTGGCTCCCAATCCAAACCCGGGGATGTTGTGATGAC 461  
Db 420 AGGTGGCGGTGGCTCGGGCGGTGGTGGTGGTGGCGGGATCTGACATTGAGCTCTC 479  
QY 462 CCCAAACCCACTCTCCCTGCTCTGTCAGTCTTGAGATCAAGCCTCCATCTCTTGAGATC 521  
Db 480 ACAGTCTCCATCTCCCTGGCTGTGTCAGCAGGAGAGAGGTCAACATGAGCTGCAAAATC 539  
QY 522 TAGTCAGAGCCTTTTACACAGTAA---TGGAATCACCTATTACATTGGTACTCTCAGAA 578  
Db 540 CAGTCAGAGTCTCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACACGAGAG 599  
QY 579 GCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAAACCGATTCTTGGGGTCCC 638  
Db 600 ACCAGGGCAGTCTCTAACTGCTGATCTATTGGGCATCCACTAGGACATCTGGGGTCCC 659  
QY 639 AGACAGGTTCACTGAGCAGTGGATCAGGACAGATTTACACTCAAGATCAGCAGAGTGA 698  
Db 660 TGATCGCTTCACAGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGA 719  
QY 699 GGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTACACGTTGG 758  
Db 720 GGCTGAAGACCTGGGCAATTTATTTACTGCAAGCAATCTTATCTCTTCGG---ACGTTGG 776  
QY 759 AGGGGGGACCAAGCTGGAATAAAA 783  
Db 777 TGGAGGCACCAAGCTCGAGATCAA 801

Search completed: May 17, 2003, 07:01:07

Job time : 46 secs

GenCore version 5.1.4 p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 17:41:10 ; Search time 1708 Seconds  
(without alignments)  
14142.464 Million cell updates/sec

Title: US-09-358-321c-31  
Perfect score: 830  
Sequence: 1 tctagaatggtgaagcgctat.....ctgaattagtagcgccgcg 830

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

GenEmbl:\*

1: gb\_ba:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_hgt\_hum:\*  
31: em\_hgt\_inv:\*  
32: em\_hgt\_other:\*  
33: em\_hgt\_mus:\*  
34: em\_hgt\_pln:\*  
35: em\_hgt\_rod:\*  
36: em\_hgt\_mam:\*  
37: em\_hgt\_vrt:\*  
38: em\_sy:\*  
39: em\_hgtgo\_hum:\*  
40: em\_hgtgo\_mus:\*  
41: em\_hgtgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

#### SUMMARIES

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	507	61.1	753	12	SCO416563 Synthetic
2	502.4	60.5	759	12	AJ250763 Mus muscu
3	501.2	60.4	1637	6	AX006750 Sequence
4	499	60.1	753	6	AX003768 Sequence
5	489	60.1	753	6	AX003776 Sequence
6	482.6	58.1	864	12	XXU31739 Single chai
7	476.6	57.4	732	12	XXU44796 Synthetic c
8	476	57.3	792	12	AF276797 Synthetic
9	411.6	49.6	768	6	AS7272 Sequence 4
10	409.4	49.3	729	6	BD009689 Anti-p53
11	407.6	49.1	749	6	AS9386 Sequence 36
12	407.6	49.1	749	6	ARI79650 Sequence
13	405.2	48.8	1611	6	AS9381 Sequence 31
14	405.2	48.8	1611	6	ARI79645 Sequence
15	404.6	48.7	729	12	ACO131532 Synthetic
16	397.2	47.9	1101	6	AS2599 Sequence 1
17	397.2	47.9	1103	6	AB2600 Sequence 2
18	392.8	47.3	795	10	MMSCFVP25 Artificial
19	389.6	46.9	738	10	AF141321 Mus muscu
20	381.6	46.0	925	6	E30617 Antibody an
21	380.4	45.8	772	6	AR085460 Sequence
22	380.4	45.8	772	6	AR088866 Sequence
23	380.4	45.8	772	6	ARI67340 Sequence
24	380.4	45.8	772	6	I36723 Sequence 33
25	380.4	45.8	772	12	SS7990 B3(Fv)-PB40
26	380.4	45.8	912	12	AB030249 Synthetic
27	370	44.6	747	6	A33046 Anti-oxazol
28	369.4	44.5	720	12	AF059737 Synthetic
29	368.8	44.4	918	6	E31219 Device for
30	368.4	44.4	804	6	A95255 Sequence 1
31	367.8	44.3	747	6	AX100176 Sequence
32	367.2	44.2	879	6	E16309 DNA encodin
33	365	44.0	774	12	UC5537 Synthetic M
34	364.6	43.9	825	12	UC65536 Synthetic M
35	364.2	43.9	726	6	AX146641 Sequence
36	362.4	43.7	864	6	A83227 Sequence 47
37	362.4	43.7	864	6	ARI82952 Sequence
38	355.8	42.9	810	10	MMU62527 Mus musculu
39	354.2	42.7	3970	12	ASY14585 Artificial
40	352.6	42.5	4363	12	SCFV18290 Expression
41	352.6	42.5	4864	12	ASY14584 Artificial
42	352.4	42.5	747	10	MMVHVKFG M.musculus
43	351.4	42.3	4661	6	AX359936 Sequence
44	351.4	42.3	4661	6	AX382150 Sequence
45	350.4	42.2	774	6	AX256288 Sequence

#### ALIGNMENTS

RESULT 1  
SCO416563  
LOCUS  
DEFINITION Synthetic construct partial mRNA for scfv antibody anti-PPV NIB  
protein.  
ACCESSION AJ416563  
VERSION AJ416563.1 GI:17978071  
KEYWORDS anti-PPV NIB protein; antibody; heavy chain; immunoglobulin superfamily; light chain; ScFv; synthetic construct; variable region.  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE artificial sequences.  
AUTHORS 1 Esteban,O., Garcia,J.A., Gorris,M.T., Dominguez,E. and Cambra,M.

Db	302	GGACTATAGGTTTGATTACTGGTACTCTCGATCTCTGGGGCCCAAGGACCACGGTCAACCG	361
QY	398	TTCTTCGAGAGGGTAAATCTCTCAGGATCTGGCTCCGAATCCAAACCCCG--GCATGTTG	454
Db	362	TTCTCTCAGTGGAGGGGTTTCAGTGGGGCGCGCTCTGGGGTGGCGGATCGAGCATG	421
QY	455	TGATGACCCCAAAACCCACTCTCCCTGCCTGTCTAGTCTTTGGAGATCAAGCCCTCCATCTCTT	514
Db	422	TGATGACCCAGTCTCCACTCTCCCTGCCTGTCTAGTCTTTGGAGATCAAGCCCTCCATCTCTT	481
QY	515	GCAGATCTAGTACAGAGCCCTTTACACAGTAAATGGAATCACTATTACATTTGGTACCTGC	574
Db	482	GCAGATCCAGTTCAGAGCCCTTGTACACAGTAAATGGGAACACCTATTACATTTGGTACCTGC	541
QY	575	AGAAGCCAGGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGG	634
Db	542	AGAAGCCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGG	601
QY	635	TCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAG	694
Db	602	TCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAG	661
QY	695	TGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTACACGT	754
Db	662	TGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTGACGT	721
QY	755	TCGGAGGGGGACCAAGCTGGAATAAAA	783
Db	722	TCGGTGGAGGGACCAAGCTGGAGCTGAAA	750
RESULT 2	SC0250763	759 bp	linear SYN 11-MAY-2000
LOCUS	SC0250763	Mus musculus synthetic construct for anti-guinea pig C5 ScFv	
DEFINITION	AJ250763	antibody, clone D10.	
ACCESSION	AJ250763.1	GI:6272278	
VERSION		antibody; heavy chain; immunoglobulin superfamily; light chain;	
KEYWORDS		ScFv; variable region.	
SOURCE		synthetic construct.	
ORGANISM		artificial sequences.	
REFERENCE		1 (bases 1 to 759)	
AUTHORS		Link, C., Hawlich, H., Meyer zu Vilsendorf, A., Gylerez, S., Nagel, E. and Koehl, J.	
TITLE		Selection of phage-displayed anti-guinea pig C5 or C5a antibodies and their application in xenotransplantation	
JOURNAL		Mol. Immunol. 38, 1235-1247 (1999)	
REFERENCE		2 (bases 1 to 759)	
AUTHORS		Link, C.	
TITLE		Direct Submission	
JOURNAL		Submitted (01-NOV-1999) Link C., Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Carl-Neuberg-Str. 1, 30625 Hannover, GERMANY	
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source		1..759	
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QY 744 TCCGTACACCTTCGGAGGGGGACCAAGCTGGAATAAAA 783
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Db 1530 TCCGTACACCTTCGGAGGGGGACCAAGCTTGAGATCAAA 1569
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RESULT 4
LOCUS AX003768
DEFINITION Sequence 62 from Patent WO9925818.
ACCESSION AX003768
VERSION AX003768.1 GI:9927571
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 753)
Kufer, P. and Raum, T.
Method of identifying binding site domains that retain the capacity
of binding to an epitope
Patent: WO 9925818-A 62 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES
source
LOCATION/Qualifiers
1..753
/organism="Mus sp."
/db_xref="taxon:10095"
BASE COUNT 174 a 184 c 216 g 179 t
ORIGIN
Query Match 60.1%; Score 499; DB 6; Length 753;
Best Local Similarity 81.7%; Pred. No. 1.6e-142;
Matches 615; Conservative 0; Mismatches 105; Indels 33; Gaps 2;

QY 64 GCGCGGTTCACCTGCAGCAGTCTGGGCTGAGCTGGTGGGCTGGGCTTCAGTGAGC 123
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QY 124 CTGTCTGCAAGCTTCGGCTACACATTTACTGACTATGAAATACACTGGGTGAGGCAG 183
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Db 61 CTGTCTGCAAGCTTCGGCTACACCTTCACAAGCTATGTTTAAAGCTGGGTGAAGCAG 120
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QY 184 ACACCTGTGCATGGCTGGAAATGGAGCTATTGATCTCTGAAACTGGTGGTACTGCC 243
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QY 244 TACAATCAGAAAGTTCAAGGACAAGGCCATAGTACTGATGACAAATCCTCCAGCAGCC 303
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Db 301 GGATCCTACGGTAGTAACACTACGACTGGTACTTCGATGTCTGGGGCCAAAGGACACGGTC 360
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QY 394 ACTGTCTCTGCA---GAGGGTAAATCTCTCAGATCTGCTCCGAATCCAAACCCGGGGAT 450
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Db 361 ACCGTCTCTCAGGTGGTGGTCTGCGGGGGGGGCTCCGGTGGTGGTCTCTAG 420
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QY 451 GTTGTGATGACCCCAACCCACTCTCCCTCCCTGTCTGAGTCTTGAGATCAAGGCTCCATC 510
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RESULT 5
LOCUS AX003776
DEFINITION Sequence 70 from Patent WO9925818.
ACCESSION AX003776
VERSION AX003776.1 GI:9927575
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 753)
Kufer, P. and Raum, T.
Method of identifying binding site domains that retain the capacity
of binding to an epitope
Patent: WO 9925818-A 70 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES
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LOCATION/Qualifiers
1..753
/organism="Mus sp."
/db_xref="taxon:10095"
BASE COUNT 171 a 188 c 215 g 179 t
ORIGIN
Query Match 60.1%; Score 499; DB 6; Length 753;
Best Local Similarity 81.7%; Pred. No. 1.6e-142;
Matches 615; Conservative 0; Mismatches 105; Indels 33; Gaps 2;

QY 64 GCGCGGTTCACCTGCAGCAGTCTGGGCTGAGCTGGTGGGCTGGGCTTCAGTGAGC 123
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Db 1 GAGGTGCAGTCTCGAGCAGTCTGGAGCTGAGCTGGGAGGCTGGGCTTCAGTGAAG 60
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QY 124 CTGTCTGCAAGCTTCGGGCTACACATTTACTGACTATGAAATACACTGGGTGAGGCAG 183
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Db 61 CTGTCTGCAAGCTTCGGGCTACACCTTCACAAGCTATGTTTAAAGCTGGGTGAAGCAG 120
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QY 184 ACACCTGTGCATGGCTGGAAATGGAGCTATTGATCTCTGAAACTGGTGGTACTGCC 243
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Db 121 AGGCTTGACAGCTCTTGGAGTGGATTTAGAGAGGTTTATCTAGAATTTGGTAATGCTTAC 180
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QY 304 TACATGGAGCTCCGAGCTGACATCTGAAGACTCTGCGCTATTACTATACAAGATGG 363
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Db 241 TCCATGGAGCTCCGAGCTGACCTGAGGACTCTGCGGTCTATTCTGTGCAAGACGG 300
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QY 364 -----TTTGAGGACTGGGGCCAAAGGACTCTGGTC 393
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Db 301 GGATCCTACGACTAACTACGACTGGTACTTCGATGTCTGGGGCCAAAGGACACGGTC 360
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QY 394 ACTGTCTCTGCA---GAGGGTAAATCTCTCAGATCTGCTCCGAATCCAAACCCGGGGAT 450
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Db 361 ACCGTCTCTCAGGTGGTGGTCTGCGGGGGGGGCTCCGGTGGTGGTCTCTAG 420
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QY 451 GTTGTGATGACCCCAACCCACTCTCCCTCCCTGTCTGAGTCTTGAGATCAAGGCTCCATC 510
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Db 421 CTCGTGATGACCCAGACTCCACTCTCCCTCCCTGTCTGAGTCTTGAGATCAAGGCTCCATC 480
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Db 481 TCCTGCAGATCTAGTCAGAGCTTTGACACAGTAATGAATCACTATTACATTGGTAC 540
Qy 571 CTGCAGAACCCAGGCGAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTTC 630
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Db 661 AGAGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAGTACACATGTTCCGTAC 720
Qy 751 ACGTTCGAGGGGGGACCAAGCTGGAAATAAAA 783
Db 721 ACGTTCGAGGGGGGACCAAGCTTGAGATCAA 753

RESULT 6
XXU31739
LOCUS XXU31739 864 bp DNA linear SYN 05-SEP-1995
DEFINITION Single chain antibody SCA 13.1 gene, complete cds.
ACCESSION U31739
VERSION U31739.1 GI:975304
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 864)
AUTHORS Nardone,F., Spano,F. and Crisanti,A.
TITLE Direct Submission
JOURNAL Submitted (17-JUL-1995) Francesco Nardone, Istituto di
parasitologia, University of Rome 'La Sapienza', Piazzale Aldo
Moro 5, Roma, RM 00185, Italy
FEATURES
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/db_xref="taxon:32630"
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Best Local Similarity 78.3%; Pred. No. 1.9e-137;
Matches 632; Conservative 0; Mismatches 139; Indels 36; Gaps 3;
Qy 46 GCGGCGCATTCGCTTTGCGGCGGTTCACACTGCAGCAGTCTGGGCTGAGCTGGTGGG 105
Db 46 GCGGCCAGCGCGGCATGCGCGAGGTTTCAGCTGCAGCAGTCTGGGCGAGAGCTTGAGG 105
Qy 106 CTTGGGCTTCAGTGAGCTGTCTCAAGGCTTCGGGCTACACATTTACTGACTATGAA 165
Db 106 TCAGGGGCTTCAGTCCAGTTGTCTGCACAGCTTCGGCTTCAACATTAAGAGCTTCTAT 165
Qy 166 ATACACTGGGTGAGGACAGACCTGTGCATGGCTGGCTGAATGGATTGGAGCTATTGATCCT 225
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Qy 226 GAAACTGGTGGTACTGCTCAATCAGAAGTTCAGGACAAAGCCATAGTACTGTAGAC 285
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Qy 286 AAATCTCTCCAGCAGAGCTACATGGAGCTCCGAGCCTGACATCTGAAGACTCTGCCGTC 345
Db 286 ACATCTCCAAACAGAGCTACCTGCAGCTCAGCGGCTGACATCTGGGGACACTGCCGTC 345
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Db 346 TATTCTGTAATGCTTAATTCTACGCTTCTCTCTGCTATGACTACTGGGCGCAAGGG 405
Qy 385 ACTCTGCTACTGTCTCTGAGAGGGTAAATCTCA---GGATCTGGCTCCGAATCAAA 441
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Qy 682 AAGATCAGCAGATGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAGTACACAT 741
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Qy 742 GTTCCGTACAGTTCGGAGGGGACCAAGCTCGAATAAAA-----AGAGAA 789
Db 766 CTTCCGTACAGTTCGGAGGGGACCAAGCTCGAATAAAA-----AGAGAA 825
Qy 790 AAATCATCTCAGAGAGGATCTGAAT 816
Db 826 AAATCATCTCAGAGAGGATCTGAAT 852
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## RESULT 7

XXU44796 732 bp mRNA linear SYN 03-FEB-1996  
 LOCUS Synthetic construct single-chain anti-acetylaminofluorene antibody  
 DEFINITION mRNA, from PCR amplified mouse VH and VL regions, partial cds.  
 ACCESSION U44796  
 VERSION U44796.1 GI:1177222  
 KEYWORDS synthetic construct.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 732)  
 AUTHORS Guesdon, J.-L. and Muller, B.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-JAN-1996) Jean-Luc Guesdon, Institut Pasteur, 28, rue du Docteur Roux, Paris, 75015, France

## FEATURES

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## misc\_feature

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## V\_region

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BASE COUNT 186 a 182 c 199 g 165 t

## ORIGIN

Query Match 57.4%; Score 476.6; DB 12; Length 732;  
 Best Local Similarity 80.6%; Pred. No. 1.3e-135;  
 Matches 586; Conservative 0; Mismatches 129; Indels 12; Gaps 2;  
 QY 69 GGTTCAACTGCAGCAGTCTGGGCTGAGCTGGTGAGCGCTTTCAGTGACGCTGTC 128  
 DB 3 GGTGCACCTGCAGCAGTCTGGGCTGAACTGGCAAACTGGGGCCTCAGTGAAGTGC 62  
 QY 129 CTGCAAGCTTCGGGCTACACATTTACTGACTATGAATAACACTGGGTGAGGACAC 188  
 DB 63 CTGCAAGCTTCGGCTACACCTTTACTACTGATGCAATCTGGGTAAACAGAGGCC 122  
 QY 189 TGTCCATGGCTCGAATGGATTGGAGCTATTGATCTCTGAACCTGGGTACTGCTACAA 248  
 DB 123 TGGACAGGGTCTGGAATGGATTGGATACATTGATCTCTAGTACTGGTTTATTAATCAA 182  
 QY 249 TCAGAAGTTCAAGGACCAAGCCATAGTACTGTAGACAAATCTCCAGCAGCAGCTACAT 308  
 DB 183 TCAGAAGTTCAAGGACCAAGCCACATTTGATCTGCAGACAAATCTCCAGCAGCAGCTACAT 242  
 QY 309 GGAGCTCCGAGCCTGACATCTGAAGACTCTGGCGTCTATTACTATACAAG----- 359  
 DB 243 GCAACTGAGCAGCCTGACATCTGAAGACTCTGACAGTCTATTACTGTGCAAGAGGAGACT 302  
 QY 360 ATGGTTTGAGACTCTGGGCGCCAGGACTCTGGTCACTGTCTCTGCA---GAGGTTAATC 416  
 DB 303 ATACGGAACTACTCTGGGGCCAAAGGACACCGTCCACCGTCTCTCTCAAGTGGAGCGGCTC 362

QY 417 CTGAGGATCTGGCTCCCAATCCAAACCCGGGATGTTGTGATGACCCCAAAACCCACTCTC 476  
 DB 363 AGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCTGAGCTCACTCACTCTCAATCTC 422  
 QY 477 CTGCGCTGTCACTCTTTGGAGATCAAGCCTCCATCTCTTCAGATCTAGTCAGAGCCTTTT 536  
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 DB 483 AACAGTAATGGAACACCTATTATTGAATGGTACCTCCAGAACCCAGGCGAGTCTCCAA 542  
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 DB 603 TGGATCAGGACAGATTTCACACTGAAATCAGCAGATGGAGGCTGAGGATTTGGGAGT 662  
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RESULT 8  
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 LOCUS Synthetic construct anti-sperm scFv antibody RASA mRNA, partial  
 DEFINITION cds.

ACCESSION AF276797  
 VERSION AF276797.1 GI:14279759  
 KEYWORDS synthetic construct.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 792)  
 AUTHORS Norton, E.J., Diekman, A.B., Westbrook, A., Flickinger, C.J. and Herr, J.C.  
 TITLE RASA, An Anti-Sperm ScFv Directed Against the Sperm Glycoform of CD52: Implications For Novel Contraceptives  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 792)  
 AUTHORS Norton, E.J., Diekman, A.B. and Herr, J.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-JUN-2000) Cell Biology, UVA, 2-27 Jordan Hall, 1300 Jefferson Park Ave., Charlottesville, VA 22908, USA  
 FEATURES Location/Qualifiers  
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 /note="derived from Mus musculus BALB/c myeloma Sp2/0 B lymphocyte hybridoma"

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 SOSLVHNSDTYLHWFLQKPGQSPPELLIRVSNRFSGVDPFRPSGSGTDTLTKLSRV  
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 BASE COUNT 174 a 204 c 229 g 185 t

## ORIGIN

Query Match 57.3%; Score 476; DB 12; Length 792;  
Best Local Similarity 80.0%; Pred. No. 2e-135;  
Matches 592; Conservative 0; Mismatches 130; Indels 18; Gaps 2;  
Qy 62 TTGGCGGCTTCACTGAGCAGCTGCTGGGCTGAGCTGGTGGGCTGGGCTTCACTGA 121  
Db 2 TGGCCAGGTGAACCTGAGCAACCTGGGTCTGAACCGGTGAGGCTTGGAGCTTCACTGA 61  
Qy 122 CGCTGTCTCGAAGGCTTTCGGGCTACACATTTACTGACTATCAATAACACTGGGTGAGGC 181  
Db 62 AGGTGCTCTGAGGCTTCTGGCTACAAATTCACACCTACTGGATGCACTGGGTGAGGC 121  
Qy 182 AGACACCTGTGATGGCTTGAATGGATGGAGCTATTGATCCTGAAACTGGTGTACTG 241  
Db 122 AGAGGCTTGGACAAGGCCCTGAGTGGATGGAGATATTATCTCTGGTGTGATTCTA 181  
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Qy 362 GG-----TTTGAGGACTGGGCGCAAGGAGCTCTGTCTACTGTCTC---TG 403  
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Qy 404 CAGAGGTAAATCTCAGGATCTGGCTCCGAATCCAAACCCGGGAGTGTGTGATGACCC 463  
Db 362 CGGGCGGCGGAGCGGTGGTGGTGTCTGGGGCGGCGGAGCGACATCAGAGCTCACTC 421  
Qy 464 CAAACCCACTCTCCCTGCTGCTAGCTCTTGAGATCAAGCTCCATCTCTTGCAGATCTA 523  
Db 422 AGTCTCCATCTCCCTGCTGCTAGCTCTTGAGGCTCCAGCTCCATCTCTTGCAGATCTA 481  
Qy 524 GTCAGAGCCTTTTACACAGTAATGAATCACTATTATTCATTTGATGCTGAGAGCCAG 583  
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Qy 584 GCCAGTCTCCAAAGCTCTGATCTTACAAAGTTTCCAAACCGATTTCTGGGCTCCAGACA 643  
Db 542 GCCAGTCTCCAGAGCTCTGATCTACAGATTTTCCAAACCGATTTTCTGGGCTCCAGACA 601  
Qy 644 GTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTCAAGATCAGAGAGTGGAGGCTG 703  
Db 602 GTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTCAAGATCAGAGAGTGGAGGCTG 661  
Qy 704 AGGATCTGGGAGTTTATTCTGCTCTCAAGTACACATGTTCCGTACACGTTCCGAGGGG 763  
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Qy 764 GGACCAAGCTGGAATAAAA 783  
Db 722 GGACCAAGCTGGAATAAAA 741

RESULT 9  
A57272  
LOCUS A57272 768 bp DNA linear PAT 03-MAR-1998  
DEFINITION Sequence 4 from Patent WO9630512.  
ACCESSION A57272  
VERSION A57272.1 GI:3713167

## SOURCE

unidentified.

unclassified.

## REFERENCE

1 (bases 1 to 768)

AUTHORS Bracco, L., Schweighoffer, F. and Tocque, B.

TITLE CONDITIONAL EXPRESSION SYSTEM

JOURNAL Patent: WO 9630512-A 4 03-OCT-1996;

COMMENT RHONE POULENC RORER SA (FR)  
Other publication AU 5402096 961016  
Other publication FR 2732348 961004.

FEATURES  
Location/Qualifiers  
source 1..768  
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BASE COUNT 181 a 185 c 218 g 184 t  
ORIGIN /db\_xref="taxon:32644"

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Best Local Similarity 73.9%; Pred. No. 1.5e-115;  
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Qy 46 GCGGCGCATTTCTGCTTTTGGCGGTTCAACTGCGAGCTCTGGGGCTGAGCTGGTGAAG 105  
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Qy 166 ATACACTGGGTGAGGCGAGACACCTGTGCTATGGCTGGGAATGGATTGGAGCTATTGATCCT 225  
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Qy 226 GAAACTGGTGGTACTGCTTACAATCAGAAGTTCAAGGACCAAGGCCATAGTACTGTAGAC 285  
Db 187 AAGAAATGGTATCTACTGAATATGCCCGAAGTTCCAGGCAAGGCCACTATGACTGCGAGC 246  
Qy 286 AAATCTCCAGCAGCAGCTACATGGAGCTCGGAGCTGACATCTGAAGACTCTGCGGTC 345  
Db 247 ACATCTCCAAATCAGGCTTACCTGAGCTCAGAGCTGGCATCTGAGGACACTGCGGTG 306  
Qy 346 TATTACTATACAAGT-----GGTTTGGAGCTGGGCGCAAGGAGCTCTGGTCACT 396  
Db 307 TATTATTTGTAATTTTACGGGGATGCTTTGGAGCTATTGGGGCGAAGGACACCGTCAAC 366  
Qy 397 GTCTCTGACAGGGTAAATCCTCA---GGATCTGGCTCCGAATCCAAACCCGGGATGTT 453  
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Qy 694 GTGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTACACG 753  
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Qy 754 TTCGAGGGGGGACCAAGCTGGAAATAAAA 783  
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## RESULT 10

BD009689

LOCUS

DEFINITION

ACCESSION

VERSION

BD009689

Anti-ps3

single-chain

antibody

fragments

and their

uses.

729 bp

DNA

linear

PAT 31-JAN-2002

GI:18638062



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KEYWORDS      JP 2001502553-A/1.
SOURCE        Spodoptera frugiperda.
ORGANISM      Spodoptera frugiperda
              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
              Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
REFERENCE     1 (bases 1 to 729)
AUTHORS       Bracco, L. and Debussche, L.
TITLE         Anti-p53 single-chain antibody fragments and their uses
JOURNAL       Patent: JP 2001502553-A 1 27-FEB-2001;
              RHONE-POULENC RORER SA
COMMENT       OS Spodoptera frugiperda
              PN JP 2001502553-A/1
              PD 27-FEB-2001
              PF 27-OCT-1997 JP 1998520119
              PR 29-OCT-1996 FR 96/13176
              PI LAURENT BRACCO, LAURENT DEBUSSCHE
              PC C07K16/18, C12N15/13, A61K39/395
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              /db_xref="taxon:7108"
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Query Match   49.3%; Score 409.4; DB 6; Length 729;
Best Local Similarity 74.8%; Pred. No. 7.2e-115;
Matches 544; Conservative 0; Mismatches 171; Indels 12; Gaps 2;
1QY 69 GGTTCAACTCAGCAGCTCTGGGCTGAGCTGGTGGAGCCCTGGGCTTCAGTGACGCTGTC 128
DB 3 GTGCGAGCTCAGCAGCTCTGGGCGAGAGCTTGTGAGTCAAGGCGCTCAGTCAAGTTGTC 62
1QY 129 CTGCAAGCTTCGGGCTACACATTTACTGACTATGAATAACACTGGGTGAGGAGACACC 188
DB 63 CTGCACAGCTCTGGCTTCAACATTAAGACTACTATATGCACTGGGTGAAGCAGAGGCC 122
1QY 189 TGTGCATGGCTCGAATGGATTGGAGCTATTGATCTCTGAACCTGGTGGTACTGCTACAA 248
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DB 303 TGGTTGGACTATTGGGGCCCAAGGGACACCGGTCACTCTCTCCTCAGGAGGCGGTTTC 362
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1QY 477 CTGCGCTGTGAGTCTTGAGATCAAGCTCCATCTCTCTTGAGATCTAGTCAGAGCCTTTT 536
DB 423 TTTGTGGTTTACCATTGGCAACACCGAGCTCCATCTCTCTTGAAGTCAAGTCAGAGCCTTT 482
1QY 537 ACAGATTAATGGAATCACTATTATTAATGGTACCTGCAGAACCGAGGCCAGTCTCCAA 596
DB 483 GGATGATGATGGAAGACATATTGAAATGGGTTGTTACAGAGCCAGGCCAGTCTCCAA 542
1QY 597 GCTCCTGATCTACAAAGTTTCCAAACCGATTCTTGGGGTCCCAAGAGGTTCACTGGCAG 656
DB 543 CGGCTAATCTATCTGGTGTCTAAACTTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAG 602
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DB 663 TTATTATTGCTGGCAAGGTACACATTTCCGCTACGTTCCGTCGCTGGCACCAGCTGGA 722
QY 777 AATAAAA 783
DB 723 AATCAAA 729
RESULT 11
LOCUS        A59386              749 bp      DNA      linear      PAT 06-MAR-1998
DEFINITION   Sequence 36 from Patent WO9704092.
ACCESSION    A59386
VERSION      A59386.1 GI:3714722
KEYWORDS     unidentified.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 749)
AUTHORS      Conseiller, E. and Bracco, L.
TITLE        P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF
JOURNAL      Patent: WO 9704092-A 36 06-FEB-1997;
              RHONE-POULENC RORER SA (FR)
COMMENT      Other publication FR 2736915 970124.
FEATURES     Location/Qualifiers
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BASE COUNT    173 a 179 c 221 g 176 t
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Query Match   49.1%; Score 407.6; DB 6; Length 749;
Best Local Similarity 74.1%; Pred. No. 2.6e-114;
Matches 547; Conservative 0; Mismatches 179; Indels 12; Gaps 2;
1QY 58 GCCTTTGGCGGCTTCAACTGCAGCAGCTCTGGGCTGAGCTGGTGGAGGCTGGGGCTTCA 117
DB 1 GCATGGCCAGCTGCAGCTGCAGAGTTCAGGGCAGAGCTTGTGGGTCAGGGGCTCA 60
QY 118 GTGACGCTGTCTCGAAGCTTCGGGCTACACATTTACTGATATGAATAACACTGGGTG 177
DB 61 GTCAAGTTGTCTCGACAGCTTCTGGCTTCAACATTAAAGACTACTATATGCACTGGTG 120
QY 178 AGGACAGACCTGTGCTGCTGGCTGGATGGATTGGAGCTATTGATCTCTGAACTGGTGT 237
DB 121 AAGCAGAGGCTCAACAGGGCTGGAGTGGATTGGATTGATCTCTGAGAATGGTGAT 180
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DB 421 ACTCCACTCACTTTGTGGTTACCATTTGCAACCAACAGCCTCCATCTCTTGCAGTCAAGT 480
QY 526 CAGAGCTTTTACAGAGTAATGGAATCACTATTATCATTTGGTACCTGCAGAACGCCAGC 585
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RESULT 12
LOCUS AR179650 749 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 46 from patent US 6326464.
ACCESSION AR179650
VERSION AR179650.1 GI:20221205
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 749)
AUTHORS Conseller, E. and Bracco, L.
TITLE P53 protein variants and therapeutic uses thereof
JOURNAL Patent: US 6326464-A 46 04-DEC-2001;
FEATURES Location/Qualifiers
source 1..749
/organism="unknown"
BASE COUNT 173 a 179 c 221 g 176 t
ORIGIN
Query Match 49.1%; Score 407.6; DB 6; Length 749;
Best Local Similarity 74.1%; Pred. No. 2.6e-114;
Matches 547; Conservative 0; Mismatches 179; Indels 12; Gaps 2;

Qy 58 GCCTTTGGGGGTTCAACTGACAGCAGTCTGGGGCTGAGCTGGTGAGGCGCTGGGGCTTCA 117
Db 1 GCCATGGCCCAAGGTGCAGTGCAGAGTCAGGGGCAGAGCTTGTGGGTGTCAGGGCGCTCA 60
Qy 118 GTGACGCTGTCTCGCAAGCTTCGGGCTACACATTTACTGACTATGAATAACACTGGGTG 177
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Db 121 AAGCAGAGGCTTGAACAGGCTGCGAGTGGATTGGATGATTGATCTCTGAGATGGTGAT 180
Qy 238 ACTGCCTACATCAGAAGTTCAAGACAAAGGCATAGTACTGTATAGACAAATCTCCAGC 297
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Qy 409 GGTAAATCCTCA---GGATCTGGCTCCGAATCCAAACCCGGGGATGTTTGTGATGACCCCA 465
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LOCUS A59381 1611 bp DNA linear PAT 06-MAR-1998
DEFINITION Sequence 31 from Patent WO9704092.
ACCESSION A59381
VERSION A59381.1 GI:3714713
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1611)
AUTHORS Conseller, E. and Bracco, L.
TITLE P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF
JOURNAL Patent: WO 9704092-A 31 06-FEB-1997;
COMMENT RHONE-POULENC FORER SA (FR)
FEATURES Other publication FR 2736915 970124.
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BASE COUNT 369 a 443 c 458 g 341 t
ORIGIN
Query Match 48.8%; Score 405.2; DB 6; Length 1611;
Best Local Similarity 74.1%; Pred. No. 1.6e-113;
Matches 544; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

Qy 62 TTGGGGGGGTTCAACTGCACAGCTCTGGGGCTGAGCTGGTGAGGCGCTGGGGCTTCACTGA 121
Db 2 TGGCCCAAGTGCAGCTGCAGGAGTCAGGGGCAGAGCTTGTGGGGTCAGGGGCGCTCACTCA 61
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Db 62 AGTTGTCTGCACAGCTTCTGGCTTCAACATTAAGACTACTATATGCACTGGGTGAGC 121
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QY 182 AGACACCTGTGCATGGCTCGAATGGATTGGAGCTATTGATCTCTGAACCTGGTGGTACTG 241  
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LOCUS AR179645 1611 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 37 from patent US 6326464.  
ACCESSION AR179645  
VERSION AR179645.1 GI:20221200  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1611)  
AUTHORS Conseiller,E. and Bracco,L.  
TITLE P53 protein variants and therapeutic uses thereof  
JOURNAL Patent: US 6326464-A 37 04-DEC-2001;  
FEATURES Location/Qualifiers  
source 1..1611  
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BASE COUNT 369 a 443 c 458 g 341 t  
ORIGIN

Query Match 48.8%; Score 405.2; DB 6; Length 1611;  
Best Local Similarity 74.1%; Pred. No. 1.6e-113;  
Matches 544; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

QY 62 TTGCGGCGGTTCAACTGCAGCAGTCTGGGGCTCAGCTGGTGGAGGCTGGGGCTTCAGTCA 121  
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QY 470 CACTCTCCCTGCTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGA 529  
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DB 602 CTGGAGTGGATCAGGACAGATTTTCACTCAAGATCAGCAGAGTGGAGGCTGAGGAT 661  
QY 710 TGGAGTTTATTCTGCTCTCAAGATCAGATGTTCCGATCAGCTTCGGAGGGGGACCA 769  
DB 662 TGGAGTTTATTCTGCTCTCAAGATCAGATGTTCCGATCAGCTTCGGAGGGGGACCA 721  
QY 770 AGCTGGAATAAAAA 783  
DB 722 AGCTGAGCTGAAA 735

RESULT 15  
LOCUS ACO131532 729 bp mRNA linear SYN 16-MAR-2000  
DEFINITION Synthetic construct for anti-p53 ScFv antibody (scFv421) containing linker sequence.

ACCESSION ACO131532  
VERSION AJ131532.1 GI:4033863  
KEYWORDS antibody; immunoglobulin superfamily; ScFv; variable region.  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 729)  
AUTHORS Caron de Fromentel,C., Gruel,N., Venot,C., Debussche,L.,  
Conseiller,E., Dureuil,C., Teillaud,J.L., Tocque,B. and Bracco,L.  
TITLE Restoration of transcriptional activity of p53 mutants in human  
tumour cells by intracellular expression of anti-p53 single chain  
Fv fragments  
Oncogene 18 (2), 551-557 (1999)  
MEDLINE 99124402  
PUBMED 9927212

REFERENCE 2 (bases 1 to 729)  
AUTHORS de Fromentel,C.  
TITLE Direct Submission  
JOURNAL Submitted (16-DEC-1998) de Fromentel C., U 380 INSERM, Institut

Cochin de Genetique Molculaire, 22 rue Mechain PARIS, 75014,  
FRANCE

# FEATURES

source

## Location/Qualifiers

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/organism="synthetic construct"

/db\_xref="taxon:32630"

/cell\_line="Pb421"

/cell\_type="hybridoma"

/focus

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/organism="Mus musculus"

/db\_xref="taxon:10090"

1..729

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/db\_xref="taxon:10090"

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/note="synthetic"

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/protein\_id="CAA10385.1"

/db\_xref="GI:4033864"

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LEWIGTDPENGDEYAPKPGKATMTADSSNTAYILQLSLASEDAVYVCFYGD  
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LDSGKTVLNLQORPGOSPRLIYLVSKLDSGVPDRFTSGSGCTDFTLKNRVEAD  
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1..116

/product="immunoglobulin heavy chain variable region"

117..131

/note="linker sequence"

132..243

/product="immunoglobulin light chain variable region"

176 a 168 c 205 g 180 t

## BASE COUNT

ORIGIN

Query Match 48.7%; Score 404.6; DB 12; Length 729;

Best Local Similarity 74.4%; Pred. No. 2.2e-113;

Matches 541; Conservative 0; Mismatches 174; Indels 12; Gaps 2;

Qy 69 GGTCAACCTGCAGCAGTCTGGGGCTGAGCTGTGAGGGCTTGGGGCTTCAGTGACCGCTGTC 128

Db 3 GGTGACGCTGCAGCAGTCTGGGGCAGAGCTTGAAGGTGAGGGGCTCAGTCAAGTTGTC 62

Qy 129 CTGCAAGCTTCGGGCTACACATTTACTGACTATGAATACACTGGGTGAGGACAGCACC 188

Db 63 CTGCACAGCTTCGGGCTCAACATTAAGACTACTATATGCACTGGGTGAGGACAGGCCC 122

Qy 189 TGTGATGGCTTGGGAATGGATGGAGCTATTGATCCTGAACTGGGTGATCTGCCTACAA 248

Db 123 TGAACAGGCTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGG 182

Qy 249 TCAGAAGTTCAAGCAAGGCGCATAGTACTGTAGCAAACTCTCCAGCAGCCTACAT 308

Db 183 CCCGAAGTTCAGGGCAAGGCGCACTATGACTGCAGACACATCCTCCAATACAGCCTACT 242

Qy 309 GGAGCTCCGAGCCTGACATCTGAAGACTCTGCCCTCTATTACTATACAAGAT----- 361

Db 243 CGAGCTCAGCAGCTGGCATCTGAGGACACTGCCGTGTATTATTGTAATTTTACGGGGA 302

Qy 362 --GGTTTCAGGACTGGGCGCAAGGACTCTGGTCTGCTCTGAGAGGGTAAATCTCTC 419

Db 303 TCCTTTGACTATTGGGGCAAGGACCAAGGTACCGTCTCCTCAGGTGAGGCGGTTTC 362

Qy 420 A---GGATCTGGCTCCGAATCAAAACCGGGGATGTGTGATGACCCCAAACTCCTC 476

Db 363 AGGCGGAGGTGCTCTGGGCGTGGCGGATCGGATGTTTTGATGACCCAACTCCACTCAC 422

Qy 477 CTTGCTGTGCTGTGGAGATCAAGCTCCATCTCTTGCAGATCTAGTCAGAGCCTTTT 536

Db 423 TTTGCGGTTACCAATTGGACAACACGAGCTCCATCTCTTGAAGTCAAGTCAGAGCCTCTT 482

Qy 537 ACACAGTAATGGAATCACCTATTATGTTGTTACTCTGCAGAAAGCCAGCCAGTCTTCCAAA 596

Db 483 GGATAGTGATGGAATAAACAATATTGTAATTGTTTACAGAGGCGCAGCCAGTCTTCCAAA 542

Qy 597 GCTCCTGATCTACAAAGTTTCCACCGATTCTCTGGGTCCTCCAGACAGGTTTCACTGGCAG 656

Db 543 CGGCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCTCCCTGACAGGTTTCACTGGCAG 602

Qy 657 TGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGT 716

Db 603 TGGATCAGGGACAGATTTCACACTTAAATCAACAGAGTGGAGGCTGAGGATTTGGGAGT 662

Qy 717 TTATTTCTGCTCTCAAAAGTACACATGTTTCGTTACACGTTTCGGAGGGGGACCAAGCTTGA 776

Db 663 TTATTTCTGCTGGCAAGGTACACATTTCTCGCTTACGTTTCGGTCTGCGCAAGCTTGA 722

Qy 777 AATAAAA 783

Db 723 AATAAAA 729

Search completed: May 17, 2003, 05:16:11

Job time : 1717 secs



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Qy 129 VTVSAEGKSGSGSEKPG-DVVMTPNPLSPVLGDAQASISCRSSQSLHNSGITYLHW 187
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Db 153 VTVSSGGGGGGGGGGGDIETQSPASLSASVGETVITTCRASN-IHN-----YLAW 207
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Qy 188 YLOKPGSPKLLIYKVNRFSGVDRPSGSGSGDTFTLKISRVEAEDLGVYFCQSOTHP 247
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Db 208 YQKQKSPQLLVNNAKTLADGVPSRFSGSGSGTQYSLKINSLOPEDFGSYCQHFWTTP 267
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Db 268 YTFGGGKLEIK 279
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Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
Query Match 40.1%; Score 558; DB 11; Length 241;
Best Local Similarity 45.6%; Pred. No. 3.2e-41;
Matches 113; Conservative 47; Mismatches 68; Indels 20; Gaps 6;
Qy 22 VOLQSQGAELVRPGASVTLSCKASGYTFDTYEHVWVROTVPVHGLEWIGIDPETGCTAYN 81
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Db 2 VKLQSQGPCLKKFGETVKISCKASGYTFDTYGNWVWVQAPGKGLKMWGINTYTGPTVA 61
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Qy 82 QKPKDAIVTVKSSSTAYMELSLTSESAVY-----YTRWFEDWGQOTLVTSAGK 136
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Db 62 DDFKGFAPFASLETASTAYLIQINNKNEDATYFCARKOLLRYFDYWGQGVTVVSSGG 121
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Qy 137 SSGSGSEKPG-DVVMTPNPLSPVLGDAQASISCRSSQSLHNSGITYLHWYLOKPGQS 195
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Db 122 GSGGGGGGGGGGDIETQSPSSLSASLGKGVITTCRASQDI-----NKVIAYOHKPGKG 176
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Qy 196 PK----LLYKVNRFSGVDRPSGSGSGDTFTLKISRVEAEDLGVYFCQSOTHPYTTG 251
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Db 177 PRSAHTLHYIQ-----PGIPSRFSGSGSGRDSFSISNLEPEDIATYYCLHYDNL-HTFG 231
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Qy 252 GGTGKLEIK 259
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Db 232 GGTGKLEIK 239
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RESULT 3
JBVC16 PRELIMINARY; PRT; 238 AA.
ID Q8VC16
AC Q8VC16;
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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
Query Match 39.8%; Score 553; DB 11; Length 238;
Best Local Similarity 95.5%; Pred. No. 8.6e-41;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 148 DVVMTNPPLSPVLGDAQASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVNRF 207
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Db 20 DVVMTQPLSPVLGDAQASISCRSSQSLVHNSGTYLHWYLOKPGQSPKLLIYKVNRF 79
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Qy 208 SGVPRFSGSGSGDTFTLKISRVEAEDLGVYFCQSOTHPYTFGGGKLEIK 259
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 SGVPRFSGSGSGDTFTLKISRVEAEDLGVYFCQSOTHPYTFGGGKLEIK 131
||||| : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 4
Q925S1 PRELIMINARY; PRT; 218 AA.
ID Q925S1
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X., Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1;
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 2.
DR NON TER 218; 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;
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Query Match 38.5%; Score 535.5; DB 11; Length 218;  
Best Local Similarity 49.5%; Pred. No. 2.7e-39;  
Matches 108; Conservative 42; Mismatches 61; Indels 7; Gaps 3;

QY 20 AAVOLQSGAELVRPQASVTLSCKASGYTFDYEHVWVQTPVHGLEWICAIIDPETGGTA 79  
DB 2 AQVKLQSGPELKPGGETVRIKSGYTFTTAGMQVQKMPGKGLUKWIGINTHSGVPK 61

QY 80 YNOKFKDKAIVTVDKSSSTAYMELRLSLTSEDSAVYYVTRW-----FEDWGQGTTLVTSAE 134  
DB 62 YAEFFKGRFAFSLTASATAYLQISNLKEDTATYCMRWYDGGFAYWGQGTTLVTSVG 121

QY 135 GKSSGSGSES KPG-DVVMTPNPPLSPVSLGDAQSISCRSSQSLHNSGITYLHWYLOKPG 193  
DB 122 GGS GSGSGSGSGSDIVLTQSPASLAVSLQORATISCRASES-VDNIGISFMNWFQOKPG 180

QY 194 QSPKLLIYKVNRFSGVDPFRFSGSGSGTDFTLKISRVE 231  
DB 181 QPPKLLIYAAKQSGGVPAAGLLASGSGTDFSLNIYPM 218

RESULT 5

Q99M37 ID Q99M37 PRELIMINARY; PRT; 238 AA.

AC Q99M37;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical 26.3 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.

QY 156 LSLPVSGLGDAQSISCRSSQSLHNSGITYLHWYLOKPGSPKLLIYKVNRFSGVDPFRS 215  
DB 1 LSLPVSGLGDAQSISCRSSQSLHNSGITYLHWYLOKPGSPKLLIYKVNRFSGVDPFRS 215

QY 216 GSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTFGGGKLEIK 259  
DB 61 GSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTFGGGKLEIK 104

RESULT 7

Q8VC55 ID Q8VC55 PRELIMINARY; PRT; 239 AA.

AC Q8VC55;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 26.3 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.

QY 148 DVVMTPNPPLSPVSLGDAQSISCRSSQSLHNSGITYLHWYLOKPGSPKLLIYKVNRF 207  
DB 20 DVVMTPNPPLSPVSLGDAQSISCRSSQSLHNSGITYLHWYLOKPGSPKLLIYKVNRF 79

QY 208 SGVPDRFSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTFGGGKLEIK 259  
DB 80 SGVPDRFSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTFGGGKLEIK 131

RESULT 6

Q9JL82 ID Q9JL82 PRELIMINARY; PRT; 104 AA.

AC Q9JL82;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

QY 142 SESKPGDVVMTNPPLSLPVLGQASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIY 201  
DB 15 SPASSDVLVTQTPSLPVLNIGQASISCKSTKSLNSDGTFLDYLWYLOKPGQSPOLLIY 74  
QY 202 KVSNRFGVDPDRFGSGSGTDFTLKISRVEAEDLVGYFCQSSTHVTYTFGGGKLEIK 259  
DB 75 LVSNRFGVDPDRFGSGSGTDFTLKISRVEAEDLVGYFCQSSTHVTYTFGGGKLEIK 132

RESULT 8  
Q8TCD0 Q8TCD0 PRELIMINARY; PRT; 239 AA.  
AC Q8TCD0;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 46.2 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=LUNG;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RW EMBL; BC022362; AAH2362.1; -  
KW Hypothetical protein  
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 33.4%; Score 464; DB 4; Length 239;  
Best Local Similarity 78.8%; Pred. No. 6.1e-33;  
Matches 89; Conservative 12; Mismatches 12; Indels 0; Gaps 0;  
QY 147 GDVMTNPPLSLPVLGQASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 206  
DB 20 GDVMTNPPLSLPVLGQASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 79  
QY 207 FSGVDPDRFGSGSGTDFTLKISRVEAEDLVGYFCQSSTHVTYTFGGGKLEIK 259  
DB 80 DSGVDPDRFGSGSGTDFTLKISRVEAEDLVGYFCQSSTHVTYTFGGGKLEIK 132

RESULT 9  
Q924R0 Q924R0 PRELIMINARY; PRT; 143 AA.  
AC Q924R0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=C57BL/6;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RW EMBL; AB067790; BAB63275.1; -  
KW InterPro; IPR003598; IG\_C2.  
DR InterPro; IPR003006; IG\_MHC.  
FT Pfam; PF00047; IG; 1.  
FT SMART; SM00408; IG2; 1.  
FT Immunoglobulin domain.  
FT NON\_TER 1  
FT NON\_TER 143  
SQ SEQUENCE 143 AA; 15869 MW; 139B2E966B81E07F CRC64;

Query Match 32.6%; Score 454; DB 11; Length 143;  
Best Local Similarity 65.7%; Pred. No. 2.2e-32;  
Matches 94; Conservative 11; Mismatches 24; Indels 14; Gaps 3;  
QY 22 VOLQSGAELVRPGASVTLSCKASGYTTDYIEIHWVROTTPVHGLEWIGALDPETGGTAYN 81  
DB 2 VOLQSGAELVRPGASVTLSCKASGYTTDYIEIHWVROTTPVHGLEWIGALDPETGGTAYN 61  
QY 82 QKFKDKAIVTDKSSSTAYMELRSLTSDSAVYYVTRWFED----WGQGLTVTVSAEKG 136  
DB 62 EKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYYCARWDEYAMDYWGQGSVTVSSE--- 119  
QY 137 SSGSGSESKPG--DVVMTNPPLS 157  
DB 120 -----SQSFPNVFPLVSCSPLS 137

RESULT 10  
Q924R6 Q924R6 PRELIMINARY; PRT; 137 AA.  
AC Q924R6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=C57BL/6;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RW EMBL; AB067783; BAB63268.1; -  
KW InterPro; IPR003006; IG\_MHC.  
FT Pfam; PF00047; IG; 1.  
FT NON\_TER 1  
FT NON\_TER 137  
SQ SEQUENCE 137 AA; 15171 MW; 5C38D966DC6A4124 CRC64;

Query Match 32.0%; Score 445; DB 11; Length 137;  
Best Local Similarity 65.9%; Pred. No. 1.3e-31;  
Matches 91; Conservative 13; Mismatches 24; Indels 10; Gaps 3;  
QY 22 VOLQSGAELVRPGASVTLSCKASGYTTDYIEIHWVROTTPVHGLEWIGALDPETGGTAYN 81  
DB 2 VOLQSGAELVRPGASVTLSCKASGYTTDYIEIHWVROTTPVHGLEWIGALDPETGGTAYN 61  
QY 82 QKFKDKAIVTDKSSSTAYMELRSLTSDSAVYYVTRWFEDWGQGLTVTVSAEKGSSGSG 141  
DB 62 EKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYYCARW-DYWGQGLTVTVSSE----- 113  
QY 142 SESKPG--DVVMTNPPLS 157  
DB 114 SQSFPNVFPLVSCSPLS 131  
RESULT 11  
Q924Q7 Q924Q7 PRELIMINARY; PRT; 145 AA.  
AC Q924Q7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;



Db 122 E-----SQSPFNVPFLVSCESPUS 140

RESULT 13

Q9DBL4 PRELIMINARY; PRT; 473 AA.

AC Q9DBL4:

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE 1810060009Rik protein.

GN IGH-1 OR 1810060009RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ON NCBI\_TaxID=10090;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;

RC MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamli M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayaashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

EMBL: AK007918; BAB25349.1; -

DR HSSP; P01842; 7FAB.

DR MGD; MGI:96443; Igh-1.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003597; Ig\_c1.

DR InterPro; IPR003600; Ig\_like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 4.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; IG\_like; 1.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.

SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 31.5%; Score 438; DB 11; Length 473;

Best Local Similarity 52.5%; Pred. No. 3.2e-30;

Matches 45; Conservative 21; Mismatches 45; Indels 20; Gaps

Qy 7 LYVLLAAAHSAFAAVALQOOSGAELVRPGASVTLSCASGYTTDTYIEIHWVQTPVHGUE 66

Db 6 VFLFLLSVTAGVHCQVLKQSGAELVKPGASVKISCKASGYTFTDYIINWVKORPGQGLE 65

Qy 67 WIGAIIDPETGCTAYNKKFKDKAIVTDKSSSTAYMELRSLTSDSASVYYTR-----WF 120

Db 66 WIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSLTSDSASVYFCALSGDYDYDF 125

Qy 121 EDWCQGLTVTVSAGEKSSGS-----GSESKPGDVV--MTPNPFLSLPVSLGDQA 166

Db 126 AYWCQGLTVTVSAAKTLATPSVYPLAPVCGGTGSSVTLGCLVKGYGPEPVTLTWNSGSL 185

Qy 167 S 167

Db 186 S 186

## RESULT 14

Q9UL80 PRELIMINARY; PRT; 114 AA.  
AC Q9UL80;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
OS (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
SEQUENCE FROM N.A.  
RP MEDLINE=98277139; PubMed=9614934;  
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035034; AAD56270.1; -.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR0031006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR NON\_TER 1  
FT NON TER 1  
FT 114 114  
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 31.5%; Score 437.5; DB 4; Length 114;

Best Local Similarity 76.1%; Pred. No. 4.6e-31;  
Matches 86; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

QY 148 DVVTPNPLSLPVSLGDPQASICRSSQSLHSGITLHLYLWYLOKPGQSPKLLIYKYSNRF 207

Db 1 DVVTSQSLPVTLRQPAISICRSSQSPYSDGNTYLVNWFQRPQSPRLLIYKYSNRD 60

QY 208 SGVPDRFSGSGGDTFTLKISRVEAEDLGVYFCQSQSTH-VPYTFGGGKLEIK 259

Db 61 SGVPDRFSGSGGDTFTLKISRVEAEDGVVYCMQGTHTWPPWTFGGGKVEIK 113

## RESULT 15

Q8VCV5 PRELIMINARY; PRT; 481 AA.  
ID Q8VCV5  
AC Q8VCV5;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 52.3 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RP TISSUE=MAMMARY TUMOR;  
RC Strausberg R.;  
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC018455; AAI18455.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR0031006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 3.  
DR SMART; SM00407; IGc1; 3.

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	534	38.4	113	1	KV2C_MOUSE	P06311 mus musculus
2	460	33.1	133	1	KV2F_HUMAN	P06310 homo sapien
3	457	32.9	113	1	KV2D_HUMAN	P01617 homo sapien
4	454	32.6	113	1	KV2E_MOUSE	P03976 mus musculus
5	454	32.6	117	1	KV2E_HUMAN	P06309 homo sapien
6	445.5	32.0	139	1	HV07_MOUSE	P01751 mus musculus
7	436	31.3	112	1	KV2D_MOUSE	P01629 mus musculus
8	435	31.3	113	1	KV2B_HUMAN	P01615 homo sapien
9	431.5	31.0	115	1	KV2A_HUMAN	P01614 homo sapien
10	431.5	31.0	137	1	HV11_MOUSE	P01755 mus musculus
11	423	30.4	138	1	HV48_MOUSE	P03980 mus musculus
12	420	30.2	113	1	KV2F_MOUSE	P01630 mus musculus
13	417.5	30.0	112	1	KV2C_HUMAN	P01616 homo sapien
14	411	29.5	117	1	HV12_MOUSE	P01756 mus musculus
15	411	29.5	117	1	HV13_MOUSE	P01757 mus musculus
16	409	29.4	117	1	HV49_MOUSE	P06328 mus musculus
17	407.5	29.3	118	1	HV51_MOUSE	P06330 mus musculus
18	405.5	29.2	120	1	HV30_MOUSE	P06329 mus musculus
19	405	29.1	117	1	HV09_MOUSE	P01753 mus musculus
20	403	29.0	120	1	HV03_MOUSE	P01747 mus musculus
21	400	28.8	140	1	HV02_MOUSE	P01746 mus musculus
22	393	28.3	136	1	HV15_MOUSE	P01759 mus musculus
23	392	28.2	117	1	HV10_MOUSE	P01754 mus musculus
24	391	28.1	117	1	HV04_MOUSE	P01748 mus musculus
25	388	27.9	113	1	KV2C_MOUSE	P01628 mus musculus
26	383.5	27.6	134	1	KV4C_HUMAN	P06314 homo sapien
27	383	27.5	133	1	KV4B_HUMAN	P06313 homo sapien
28	382.5	27.5	114	1	KV4A_HUMAN	P01625 homo sapien
29	381	27.4	112	1	KV2A_MOUSE	P01626 mus musculus
30	381	27.4	117	1	HV05_MOUSE	P01749 mus musculus
31	381	27.4	117	1	HV14_MOUSE	P01758 mus musculus
32	380	27.3	117	1	HV06_MOUSE	P01750 mus musculus
33	376.5	27.1	108	1	KV1_CANFA	P01618 canis famil

```

RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RR "Amino acid sequence of a kappa Bence Jones protein from a case of
RL primary amyloidosis.";
RL Biochemistry 12:3763-3780(1973).
RN [2]
RN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RR MEDLINE=73166638; PubMed=4700495;
RR Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RA "Structural identity of Bence Jones and amyloid fibril proteins in a
RL patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281(1973).
CC -!- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC PIR: AO1888; K2HUTW.
DR DR
DR HSSP; PO1607; IREI.
DR InterPro; IPR0031006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 32.9%; Score 457; DB 1; Length 113;
Best Local Similarity 76.8%; Pred. No. 2.3e-31;
Matches 86; Conservative 13; Mismatches 13; Indels 0; Gaps

QY 148 DVMTNPPLSPVLSLGDQAISICRSQSLLSHNGITYLHWYLQKPGSPKLLIYKVSNRF 2070
DDB 1 DIVMTPSLPVPTGEPASISCRSSQSLLSDGFNYLNWLQKPGSPZLLIYALSNRA 60
QY 208 SGVPDRFGSGSGDTFTLKISRVAEDLGWVCFSOSTHPVTFGGTKLEIK 259
DDB 61 SGVPDRFGSGSGDTFTLKISRVAEDGVGYTCMALQAPITFGGTRLEIK 112

RESULT 4
IID KV2E MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DD 23-OCT-1986 (Rel. 02, Created)
DDT 23-OCT-1986 (Rel. 02, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxId=10090;
PI [1]
RP SEQUENCE.
RR TISSUE=Hybridoma;
RC MEDLINE=85128968; PubMed=6441768;
RA Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RR "Mature V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6
RL origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RT Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -!- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
CC PIR: AO1912; KVM517.
```

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DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 123 93
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 32.6%; Score 454; DB 1; Length 113;
Best Local Similarity 75.9%; Pred. No. 4.1e-31;
Matches 85; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDOASISCRSSQSLHSHNGITLYLHWYLOKPGQSPKLLIYKVSNR 207
DB 1 DIVMTQAVFSNPVLGTSAISCRSSKSLHSHNGITLYLWYLOKPGQSPQLLYQMSNLA 60

QY 208 SGVDPDRFSGSGGDTFTLKISRVAEDLGVCSTHVPYTFGGGKLEIK 259
DB 61 SGVDPDRFSGSGGDTFTLRISRVAEDGVVYCAHNLPLPYTFGGGKLEIK 112

RESULT 5
KV2E HUMAN ID ID_KV2E HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 309:73-76(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT NON TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117
FT DOMAIN 5 27
FT DOMAIN 28 43
FT DOMAIN 44 58
FT NON TER 59 65
IG KAPPA CHAIN V-II REGION GM607.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.

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FT DOMAIN 66 97
FT DOMAIN 98 106
FT DOMAIN 107 116
FT DISULFID 27 97
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 32.6%; Score 454; DB 1; Length 117;
Best Local Similarity 77.9%; Pred. No. 4.3e-31;
Matches 88; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 147 GDVMTNPPLSLPVSLGDOASISCRSSQSLHSHNGITLYLHWYLOKPGQSPKLLIYKVSNR 206
DB 4 GDVMTQSPSLPVTPTGEPASISCRSSQSLHSHNGVYLDWYLOKPGQSPQLLYLGSNR 63

QY 207 FSGVDPDRFSGSGGDTFTLKISRVAEDLGVCSTHVPYTFGGGKLEIK 259
DB 64 ASGVDPDRFSGSGGDTFTLKISRVAEDGVVYCMQGLQTPQTFGGGKVEIK 116

RESULT 6
HV07 MOUSE ID ID_HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.B.M., Faskind M., Reich M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -! MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL; J00529; AAA38170.1; -.
DR PIR; A02034; MHMS18.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 124
FT DOMAIN 125 139
FT DISULFID 41 115
FT NON TER 139 139
IG HEAVY CHAIN V REGION B1-8/186-2.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

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RESULT 8  
KV2B\_FUMA  
ID\_KV2B

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RL  Naturwissenschaften 56:195-205(1969).
CC  -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC  -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR  PIR; A01885; K2HUCM.
DR  HSSP; P01607; IREI.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Ig; 1.
KW  Immunoglobulin v region; Bence-Jones protein.
FT  DISULFID 24 95
FT  NON TER 115 115
SQ  SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 31.0%; Score 431.5; DB 1; Length 115;
Best Local Similarity 75.2%; Pred. No. 3.1e-29;
Matches 85; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 148 DVMTPTPLSLPVSIGDQASISCRSSQSLHLS-NCITVYHMYLQKPGOSPLLYKYVSNR 206
DB 2 DIVMTQTPLSLPVTGPEPASISCRSSQSLDSDGNTYLNWYLOKAGOSPLLTYLSYR 61

QY 207 FSGVDFRFGSGSGTDFTLKISRVAEADLGVYFCQSQTHVPYTFGGGTGLEIK 259
DB 62 ASGVDFRFGSGSGTDFTLKISRVAEDVGVYCMQRLIEIPYTFGGGTGLEIR 114

RESULT 10
HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00539; AAA38172.1; --
CC PIR; A02038; G2MS43.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Ig; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 127
FT DOMAIN 128 138
FT DISULFID 41 115
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 30.4%; Score 423; DB 1; Length 138;
Best Local Similarity 63.5%; Pred. No. 2e-28;
Matches 87; Conservative 14; Mismatches 28; Indels 8; Gaps 2;

QY 3 SAIVLVYVLLAAAHSAFAAVQLQSGAELVRPGASVTLSCKASGYTFTDYEIHVWROTPV 62
DB 4 SYILLF--LVATATDVHSQVQLQPGAEVLVKGASVQLSCKASGHTFTNYIHWKQRP 61

QY 63 HGLEWIGAIIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRSLTSDSAVYVY---- 117
DB 62 RGLEWIGRIDPNSGTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSDSAVYVCARYL 121

RESULT 11
HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an Igo-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138
FT DOMAIN 21 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 127
FT DOMAIN 128 138
FT DISULFID 41 115
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 30.4%; Score 423; DB 1; Length 138;
Best Local Similarity 63.5%; Pred. No. 2e-28;
Matches 87; Conservative 14; Mismatches 28; Indels 8; Gaps 2;

QY 3 SAIVLVYVLLAAAHSAFAAVQLQSGAELVRPGASVTLSCKASGYTFTDYEIHVWROTPV 62
DB 4 SYILLF--LVATATDVHSQVQLQPGAEVLVKGASVQLSCKASGHTFTNYIHWKQRP 61

QY 63 HGLEWIGAIIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRSLTSDSAVYVY---- 117
DB 62 RGLEWIGRIDPNSGTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSDSAVYVCARYL 121

```

-	-	MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
-	-	PROTEIN HAS ALSO BEEN DETERMINED.
-	-	MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
PIR	A02039	MHMS4E.
HSSP	P01789	LMCP.
InterPro	IPR003006	Ig_MHC.
InterPro	IPR003596	Ig_v.
Pfam	PF00047	Ig_1.
SMART	SM00406	Ig_v; 1.
Immunoglobulin	V region	Glycoprotein.
DISULFID	22	BY SIMILARITY.
CARBOHYD	55	N-LINKED (GLCNAC. . .) (COMPLEX).



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FT NON TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match          29.5%; Score 411; DB 1; Length 117;
Best Local Similarity 69.8%; Pred. No. 1.6e-27;
Matches 81; Conservative 12; Mismatches 19; Indels 4; Gaps 1;

QY 22 VLOQSGAELVPCASVTLSCASGYTFTDYEHVHVRQTPVHGLEWICAIIDPETGGTAYN 81
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VLOQSGPELVKPGASVKMSCKASGYTFTDYIMKWKVKQSHGKSLWIGDINPNNGGTSYN 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 82 QKFKDKAIVTVDKSSSTAYMELRLSLTSEDSAVYY----YTRWPEEDMGOGTLVTYSA 133
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 QKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWFYDVGAGTTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
HV13 MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DISULFID 22 96
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match          29.5%; Score 411; DB 1; Length 117;
Best Local Similarity 69.8%; Pred. No. 1.6e-27;
Matches 81; Conservative 12; Mismatches 19; Indels 4; Gaps 1;

QY 22 VLOQSGAELVPCASVTLSCASGYTFTDYEHVHVRQTPVHGLEWICAIIDPETGGTAYN 81
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VLOQSGPELVKPGASVKMSCKASGYTFTDYIMKWKVKQSHGKSLWIGDINPNNGGTSYN 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 82 QKFKDKAIVTVDKSSSTAYMELRLSLTSEDSAVYYTR----WPEEDMGOGTLVTYSA 133
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 QKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWFYDVGAGTTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

GenCore version 5.1.4 ps 4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 14:21:35 ; Search time 44 Seconds  
(without alignments)  
587.731 Million cell updates/sec

Title: US-09-358-321c-32  
Perfect score: 1391  
Sequence: 1 MVSAILVYVLLAAAHSAFA.....FGGKLEIKKEKLISEDL 269

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 73:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	748.5	53.8	249	2 S41374	single chain Fv an
2	662.5	47.6	268	2 A56446	Ig heavy chain V r
3	636.5	45.8	233	2 JC5322	p53 specific singl
4	563	40.5	112	2 E27887	Ig kappa chain V r
5	562	40.4	112	2 S32189	Ig kappa chain V r
6	558	40.1	118	2 PT0359	Ig kappa chain V r
7	558	40.1	131	2 B34904	Ig kappa chain pre
8	554	39.8	112	2 D27887	Ig kappa chain V r
9	554	39.8	112	2 S53750	antibody Fab Jel 1
10	554	39.8	115	2 S60066	Ig kappa chain V r
11	554	39.8	131	2 B32513	Ig kappa chain pre
12	554	39.8	131	2 C34904	Ig kappa chain pre
13	552	39.7	111	2 PL0257	Ig kappa chain V r
14	552	39.7	112	2 A27887	Ig kappa chain V r
15	551	39.6	115	2 S38715	Ig kappa chain V r
16	551	39.6	131	2 S30577	Ig kappa chain pre
17	549	39.5	112	2 E27887	Ig kappa chain V r
18	547	39.3	112	2 B31485	Ig kappa chain V r
19	547	39.3	113	2 B41940	Ig light chain V r
20	546	39.3	112	2 C27887	Ig kappa chain V r
21	544	39.1	131	2 C34903	Ig kappa chain pre
22	542	39.0	131	2 D34904	Ig kappa chain pre
23	541	38.9	112	2 A49715	Ig kappa chain V r
24	538	38.7	131	2 PT0178	Ig kappa chain pre
25	537	38.6	131	2 D29380	Ig kappa chain pre
26	534	38.4	113	1 KWS26	Ig kappa chain V r
27	534	38.4	113	2 PL0205	anti-DNA autoantib
28	534	38.4	132	2 PH0106	anti-digoxin trans
29	534	38.4	219	2 S16112	Ig kappa chain V r

30	531	38.2	131	2 S52449	Ig kappa chain V r
31	529	38.0	112	2 A31807	Ig kappa chain V r
32	527	37.9	131	2 B39276	Ig light chain pre
33	526	37.8	107	2 D32530	Ig kappa chain V r
34	524	37.7	110	2 S26335	Ig kappa chain V r
35	523	37.6	113	2 PL0203	anti-DNA autoantib
36	522	37.5	217	2 S42772	Ig kappa chain - m
37	522	37.5	219	2 S52028	Ig kappa chain - m
38	521	37.5	219	2 PC4203	Ig kappa chain (mo
39	520	37.4	219	2 S38865	Ig kappa chain - m
40	519.5	37.3	130	2 C29380	Ig kappa chain pre
41	519	37.3	112	2 F27887	Ig kappa chain V r
42	513	36.9	112	2 S38719	Ig light chain V r
43	512	36.8	103	2 PH1030	Ig light chain V r
44	512	36.8	108	2 S32530	Ig kappa chain V r
45	510	36.7	114	2 A32967	Ig kappa chain V - I

ALIGNMENTS

RESULT 1

S41374  
single chain Fv antibody - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C;Accession: S41374  
R;Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A;Description: Construction and functional characterization of a single chain Fv antibody  
A;Reference number: S41374  
A;Accession: S41374  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-249 <ART>  
A;Cross-references: EMBL:229480

Query Match 53.8%; Score 748.5; DB 2; Length 249;  
Best Local Similarity 61.1%; Pred. NO. 1.4e-48;  
Matches 151; Conservative 29; Mismatches 56; Indels 11; Gaps 3;

QY	22	VOIQSGAEILVRPGASVTLSCKASGYTFTDYEIHWRVOTPVHGLEWIGAIIDPETGGTAYN	81
DB	2	VOIQSGAEILVRPGASVKUSCTASGTFNFKDDYIHWRVOTPVHGLEWIGAIIDPETGGTAYN	61
QY	82	QKFKDAIVTVDKSSSTAYMELRLTSEDSAVYYTRWTFED-----WGQGTFLVTVSA	133
DB	62	PRQDKATITADTSSNTAYLLSLTSEDTAVYYCAR--RDTLYTSLGYWGQGSTVTVSS	119
QY	134	EGKSSGSGSESKPG-DVVMTPNPLSPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKP	192
DB	120	RGSGSGSGSGGGGSDIELTQSPSPVVIIPGESVSIKSCRSKSLLYSDGSLFWFLQRP	179
QY	193	GQSPKLLIYKSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVFCFSOSTHPVPTFGG	252
DB	180	GQSPQLLIYRMSLNSLGVDRFSGSGSGTFTLRISVEAEDGVVYTCMHREYPLTIGA	239
QY	253	GTKLEIK 259	
DB	240	GTKLEIK 246	

RESULT 2

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C;Accession: A56446  
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical  
A;Reference number: A56446; MUID:95229583; PMID:7713873  
A;Accession: A56446



C;Comment: This protein is an anti-double-stranded DNA antibody.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;19-98/Domain: immunoglobulin homology <IMM>

Query Match 40.1%; Score 558; DB 2; Length 118;  
Best Local Similarity 95.5%; Pred. No. 8.7e-35;  
Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207  
DB 4 DVVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLYLHWYLOKPGQSPKLLIYKVSNR 63

QY 208 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 259  
DB 64 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 115

RESULT 7  
B34904  
Ig kappa chain precursor V region (12-40 and 5-14) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 21-Jul-2000  
C;Accession: B34904; H34903  
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A;Title: Active site structure and antigen binding properties of idiotypically cross-reactive V region of mouse Ig kappa chain precursor V region (12-40 and 5-14)  
A;Reference number: A34903; MUID:90094387; PMID:2104617  
A;Accession: B34904  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA

A;Residues: 1-131 <BED>  
A;Cross-references: GB:M32384; GB:J05237; GB:J05238; MID:9639656; PIDN:AAA61589.1; PID:G34904  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 40.1%; Score 558; DB 2; Length 131;  
Best Local Similarity 95.5%; Pred. No. 9.8e-35;  
Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207  
DB 20 DVVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLYLHWYLOKPGQSPKLLIYKVSNR 79

QY 208 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 259  
DB 80 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 131

RESULT 8  
D27887  
Ig kappa chain V region (H36-2) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 21-Jan-2000  
C;Accession: D27887  
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A;Title: Structural and functional implications of a restricted antibody response to a dominant epitope of the myeloma protein 357  
A;Reference number: A91043; MUID:8630656; PMID:2427335  
A;Accession: D27887  
A;Molecule type: DNA

A;Residues: 1-112 <CAT>  
A;Experimental source: strain Balb/c  
A;Note: This sequence was determined from the germline gene  
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus H5N1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 112;  
Best Local Similarity 94.6%; Pred. No. 1.6e-34;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207  
DB 1 DVVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLYLHWYLOKPGQSPKLLIYKVSNR 60

QY 208 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 259  
DB 61 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 112

RESULT 9  
S53750  
antibody Fab Jel 103 light chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jan-2000  
C;Accession: S53750  
R;Pokkuluri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.  
J. Mol. Biol. 243, 283-297, 1994  
A;Title: Preparation, characterization and crystallization of an antibody Fab fragment (1-103) of anti-mouse IgG1 antibody  
A;Reference number: S53750; MUID:95018269; PMID:7523684  
A;Accession: S53750  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <POK>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 112;  
Best Local Similarity 95.5%; Pred. No. 1.6e-34;  
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207  
DB 1 DVVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLYLHWYLOKPGQSPKLLIYKVSNR 60

QY 208 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 259  
DB 61 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 112

RESULT 10  
S60066  
Ig kappa chain V region (monoclonal antibody C3) (validated) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Feb-1996 #sequence\_revision 10-Oct-1997 #text\_change 23-Mar-2001  
C;Accession: S60066  
R;Wien, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.; Hogle, J.E.  
Nat. Struct. Biol. 2, 232-243, 1995  
A;Title: Structure of the complex between the Fab fragment of a neutralizing antibody (C3) and the antigen (H36-2) of the myeloma protein 357  
A;Reference number: S60066; MUID:95292109; PMID:7539711  
A;Accession: S60066  
A;Molecule type: mRNA  
A;Residues: 1-115 <WIE>  
A;Cross-references: EMBL:X84697; NID:G773226  
R;Wien, M.W.; Hogle, J.E.  
Submitted to the Brookhaven Protein Data Bank, January 1995  
A;Reference number: A52979; PDB:1FPT  
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-23, 'S', 25-115  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>  
F;23-93/Disulfide bonds: #status experimental

Query Match 39.8%; Score 554; DB 2; Length 115;  
Best Local Similarity 95.5%; Pred. No. 1.7e-34;  
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207  
DB 1 DVVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLYLHWYLOKPGQSPKLLIYKVSNR 60

QY 208 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 259  
DB 61 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSOSTHVPVTFGGGKLEIK 112

```

RESULT 11
B32513
IG kappa chain precursor V region (MRL4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: B32513
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: A94689; MUID:8831394; PMID:3138286
A:Accession: B32513
A:Molecule type: DNA
A:Residues: 1-131 <GB>
A:Cross-references: GB:M20828; NID:g196937; PIDN:AAA38843.1; PID:g196938
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 131;
Best Local Similarity 95.5%; Pred. No. 2e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 20 DVVMTQTPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 79
QY 208 SGVPRDFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPYTFGGGKLEIK 259
DB 80 SGVPRDFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPYTFGGGKLEIK 131

RESULT 12
C34904
IG kappa chain precursor V region (3-24) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C:Accession: C34904; I31485
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-re
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: C34904
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
R:Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A:Title: Comparison of variable region primary structures within an anti-fluorescein idi
A:Reference number: A31485; MUID:89109167; PMID:2492278
A:Accession: I31485
A>Status: preliminary
A:Molecule type: protein
A:Residues: 20-52 <BE2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 131;
Best Local Similarity 94.6%; Pred. No. 2e-34;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 20 DVVMTQTPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 79
QY 208 SGVPRDFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPYTFGGGKLEIK 259
DB 80 SGVPRDFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPYTFGGGKLEIK 131

RESULT 13
B32513
IG kappa chain precursor V region (MRL4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: B32513
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: A94689; MUID:8831394; PMID:3138286
A:Accession: B32513
A:Molecule type: DNA
A:Residues: 1-131 <GB>
A:Cross-references: GB:M20828; NID:g196937; PIDN:AAA38843.1; PID:g196938
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 131;
Best Local Similarity 95.5%; Pred. No. 2e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 20 DVVMTQTPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 79
QY 208 SGVPRDFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPYTFGGGKLEIK 259
DB 80 SGVPRDFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPYTFGGGKLEIK 131

RESULT 14
A27887
IG kappa chain V region (H37-60) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: A27887
R:Caeton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: A27887
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was isolated from a hybridoma protein that binds influenza virus h
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 39.7%; Score 552; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 2.3e-34;
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 1 DVVMTQTPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 60
QY 208 SGVPRDFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPYTFGGGKLEIK 259
DB 61 SGVPRDFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPYTFGGGKLEIK 111

RESULT 15
S38715
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
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Search completed: May 16, 2003, 14:26:15  
Job time : 45 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

DM protein - protein search, using sw model

Run on: May 16, 2003, 14:25:30 ; Search time 68 Seconds  
(without alignments)  
381.548 Million cell updates/sec

File: us-09-358-321c-32

Perfect score: 1391  
Sequence: 1 MVSATLVYLLAAAHSAFA.....FGGTTKLEIKELISEDL 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Total number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	927.5	66.7	252	9	US-09-887-853-4
2	823.5	59.2	253	9	US-09-880-748-1964
3	818.5	58.8	260	9	US-09-782-672-2
4	793	57.0	331	9	US-10-059-261-169
5	788	56.6	535	9	US-09-968-851-38
6	740.5	53.2	281	9	US-10-112-788-9
7	730	52.5	258	9	US-10-247-488-4
8	730	52.5	260	9	US-09-880-748-1039
9	727	52.3	256	9	US-10-247-488-2
10	719	51.7	262	9	US-09-880-748-2081
11	718	51.6	244	9	US-09-880-748-1991
12	709.5	51.0	244	10	US-09-940-391-1
13	708	50.9	245	9	US-09-991-470-27
14	706.5	50.8	245	9	US-09-880-748-1902
15	706	50.8	248	9	US-09-880-748-1778
16	700.5	50.4	381	10	US-09-822-698A-5
17	696	50.0	248	9	US-09-880-748-1104
18	696	50.0	248	9	US-09-880-748-1717
19	696	50.0	250	9	US-09-880-748-932

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20 695.5 50.0 239 9 US-10-151-882-23
21 695.5 50.0 249 9 US-09-880-748-1635
22 692 49.7 239 9 US-10-162-889-6
23 692 49.7 239 10 US-09-808-037-6
24 690.5 49.6 243 9 US-09-880-748-2063
25 689 49.5 248 9 US-09-880-748-1733
26 688 49.5 248 9 US-09-880-748-1008
27 687.5 49.4 241 9 US-09-880-748-1948
28 686 49.3 248 9 US-09-880-748-1446
29 685 49.2 248 9 US-09-880-748-1719
30 685 49.2 248 9 US-09-880-748-1737
31 684.5 49.2 245 9 US-09-880-748-1900
32 684.5 49.2 249 9 US-10-237-667-18
33 684.5 49.2 249 9 US-10-237-708-18
34 684.5 49.2 249 9 US-10-237-866-18
35 684.5 49.2 249 9 US-10-237-871-18
36 684.5 49.2 249 9 US-10-237-624-18
37 684.5 49.2 249 10 US-09-984-186-18
38 684 49.2 242 9 US-09-880-748-1580
39 683 49.1 237 10 US-09-924-099-9
40 683 49.1 243 10 US-09-924-099-10
41 683 49.1 248 9 US-09-880-748-1879
42 682.5 49.1 250 9 US-09-887-853-2
43 682.5 49.1 288 10 US-09-818-247-22
44 680 48.9 248 9 US-09-880-748-1700
45 679.5 48.8 240 10 US-09-976-787-28
```

#### ALIGNMENTS

#### RESULT 1

US-09-887-853-4  
Sequence 4, Application US/09887853  
Patent No. US20020168375A1  
GENERAL INFORMATION:

APPLICANT: Huston, James S.  
Oppermann, Hermann  
Houston, L. L.  
Ring, David B.

TITLE OF INVENTION: Biosynthetic Binding Proteins For Imaging

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/887,853

FILING DATE: 21-Jun-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/133,804

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kelley, Robin D.

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477

TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 amino acids

TYPE: amino acid

[illegible]

Query Match 66.7%; Score 927.5; DB 9; Length 252;  
Best Local Similarity 76.6%; Pred. NO. 9.2e-51;  
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps

22 VQLQSGAELVRPGASVLTLSCKASGYFTDYEIHWQRTPVHGLEWIGAIIDPETGCTAYN 81  
||||| ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||  
3 VQLQSGPELVKPGASVRNSCKSSGYIFTDFYMNWRQSHGKSLDYGIVISPSYGVGTGYN 62

```
82 QKFQKAIIVTDKSSSTAYMELRSLTSDSAVYYY-----TRWFED-WGQGTLVTVAEG 135
      ||||| : ||||||| ||||||| ||||||| | : ||| : ||||| :
63 QKFQKGATLTVDKSSSSTAYMELRSLTSDSAVYYCACSSGNKNAMDYWGHGCAVTVSSSG 122
```

136 KSSGSGSEKPGDVMTNPPLSPVSLGDAQISCRSSQSLHNSGITYLHWYLOKPGQS 195  
123 -SSSGSSSSGSDVMTOTPLSPVSLGDAQISCRSSQSLVHNSGNTYLNWYLOKAGOS 181

196 PKLLIYKVNRESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTEGGTK 255  
|||||  
182 PKLLIYKVNRESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTEGGTK 241  
|||||

256 LEIK 259  
|||  
242 LEIK 245

RESULT 2  
IS-09-880-748-1964

Sequence 1964, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 60/212,210  
 PRIOR FILING DATE: 2000-06-15  
 PRIOR APPLICATION NUMBER: 60/240,816  
 PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/277,379  
 PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/233,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 1239  
COMPLET. 04/04/2002 12:00

SEQ ID NO 1964  
LENGTH: 253  
TYPE: PRT

S-09-880-748-1964

Query Match 59.2%; Score 823.5; DB 9; Length 253;

Y 22 VQLQSGAELVRPGASVTLSCRKASGYTFTDYEIHWVRQTPVHGLEWICAIDPETGGTAYN 81  
Matches 164; Conservative 27; Mismatches 47; Indels 13; Gaps

b 2 VQLQSGAEVKEPGASVKVCKASGYTFTSYGISWVRQAPGQGLENNGWISAYNGNTNYA 61

py 82 QKPKDKAIIVTDKSSSTAYMELRSLTSDSAVYYVTR-----WFDWGQGTLTVT 131

62 QKLQGRVTMTTDTSTAYMELSLRSDDTAVYCARNPYYDSSEGFEDYWGQTMVTV 121

132 SAEGKSSGSGSESKPG---DVVMTNPPLSLPVLGPOASISCRSSOSLHNSGITYLHWY 188

b' 122 SGGGCGGGSGGGGSGALDVMTQSPPLPVTLGQPASISCRSSQLVYSDGNTYLWF 181

Qy 189 LQKPGOSPLLIIYKVNSRFGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCSQSTHPV 248  
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::  
Db 182 OORPGOSPRLIYKVNSRNDSVPDRFSGSGGTDFTLKISRVEADRVGYVCWOATRWDF 241  
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Qy 249 TFGG<sup>+</sup>TKLEIK 259  
||| ||| : |||  
Db 242 TFGQGT<sup>+</sup>KMEIK 252

RESULT 3  
US-09-782-672-2

Publication No. US20030036092A1  
 GENERAL INFORMATION:  
 APPLICANT: Iverson, Brent

Georgiou, George  
Chen, Gang  
Olsen, Mark J.  
Daugherty, Patrick

; TITLE OF INVENTION: Directed  
 ; Antibodies  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TEXAS

COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:

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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: PatentIn Release
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; APPLICATION NUMBER: US/0  
; FILING DATE: 12-Feb-2001  
; CLASSIFICATION: <Unknown>

APPLICATION NUMBER: 08/8  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 37,  
REFERENCE/DOCKET NUMBER  
TELECOMMUNICATION INFORMATION

TELEFAX: (713) 789-2679  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-09-782-672-2  
Query Matched 58.8%; Score

QY 22 VQLQOSGAELVRPGASVTLSCKASGYTFE

Db	2	VQLQQSGPELVKPGASVRMSCKSSGYIF
Ov	82	OKFKDKAIVTVDKSSSTAYMELRSLTSEE

Db	62	QKFKGKATLTVDKSSSTAYMELRSLTSEE
Ov	136	KSSGSGSESKEPG-DWMTNPISLPVSI

Db 122 GGSGGGGGGGSDIVLTQSPASLAVSL



QY 195 SPKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEADLGVYFCSQSTHVPYTFGGT 254  
DB 182 PKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEADLGVYFCSQSTHVPYTFGGT 241  
QY 255 KLEIK 259  
DB 242 KLEIK 246

RESULT 4  
US-10-059-261-169  
Sequence 169, Application US/10059261  
Publication No. US20030077826A1  
GENERAL INFORMATION:  
APPLICANT: EDELMAN, LENA  
APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS  
APPLICANT: BRIAND, JEAN-PAUL  
TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET  
SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC  
FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX  
(PTPC)  
FILE REFERENCE: 03495, 0216  
CURRENT APPLICATION NUMBER: US/10/059,261  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 60/265,594  
PRIOR FILING DATE: 2001-02-02  
NUMBER OF SEQ ID NOS: 325  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 169  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-ScFv350  
peptide sequence  
US-10-059-261-169

Query Match 57.0%; Score 793; DB 9; Length 331;  
Best Local Similarity 59.2%; Pred. No. 2.6e-42;  
Matches 167; Conservative 28; Mismatches 59; Indels 28; Gaps 4;  
QY 1 MVSAILVYLLAAAHSAFAA-----VOLQSGAELVPRPGASVTLSC 43  
DB 49 MVSAILVYLLAAAHSAFAADLGHSHHHHIEGREFQVOLQSGAELAKPGASVKLSCK 108  
QY 44 ASGYTFDIHWRQTPVHGLEWIGAIIDPETGTATYNOXKFKDAIUTVDKSSSTAYMEL 103  
DB 109 ASGHTFTSYMMHWVKORPGOGLEWIGVINLSSGYIKYNOEFKDKATLTADKSNATYMH 168  
QY 104 RSLTSEDSAVVYTR-----WFDWGGGTLVTSAGKSGSGSEKPG-DVWVTPNPLS 157  
DB 169 SLLTYEDSAVYCARAAQATTFDWGGGTLVTSAGKSGSGSGGSDIWMQSHKF 228  
QY 158 LPVSLGPOASISCRSSOSLHNSGITYLHWYLOKPGOSPKLLIYKVNRFSGVDPDRFSGS 217  
DB 229 MSTSVGRVSITKASQDV-----STAUGVYQKPGOSPKLLIYWASTRUTGVPDRFTGS 283  
QY 218 GSGTDFTLKLISRVEADLGVYFCSQSTHVPYTFGGGTLKLEIK 259  
DB 284 GSGTDYTLTSSVQAEADLALYCOQHYSPTPTFGGGLKGIK 325

RESULT 5  
US-09-968-851-38  
Sequence 38, Application US/09968851  
Publication No. US20020193561A1  
GENERAL INFORMATION:  
APPLICANT: CONSEILLER, EMMANUEL  
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
USES THEREOF  
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:  
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
DUNNER, LLP  
STREET: 1300 I Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/968,851  
FILING DATE: 03-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,035  
FILING DATE: 20-Feb-1998  
APPLICATION NUMBER: PCT/FR96/01111  
FILING DATE: 17-JUL-1996  
APPLICATION NUMBER: FR 95/08729  
FILING DATE: 19-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Strauss, William L.  
REGISTRATION NUMBER: 47,114  
REFERENCE/DOCKET NUMBER: 03804.0142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-968-851-38

Query Match 56.6%; Score 788; DB 9; Length 535;  
Best Local Similarity 65.2%; Pred. No. 8.4e-42;  
Matches 159; Conservative 24; Mismatches 57; Indels 4; Gaps 2;  
QY 20 AAVOLOQSGAELVPRPGASVTLSCASGYTFTDYEIHWVRQTPVHGLEWIGAIIDPETGGTA 79  
DB 2 AVOLOESGAELVSGASVKLSCTASGFNIKDYMMHWVKORPEQGLEWIGWIDPENGDTG 61  
QY 80 YNOKFQKDAIUTVDKSSSTAYMELRSLTSEDSAVVY---YTRWFEDWGGGTLVTVSAGK 136  
DB 62 YAPKFOGKATMTADTSSNTAYLQLSLASEDTAVVYCNFYGDALDYWGQCTTVTVSSGGG 121  
QY 137 SSGSGSEKPG-DVWVTPNPLSIPVSLGPOASISCRSSOSLHNSGITYLHWYLOKPGOS 195  
DB 122 GSGGGSGGGGSDVLTMTQTPLTLSVTIGOPASISCKSSOSLSDSGKTYLNLQRPQOS 181  
QY 196 PKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEADLGVYFCSQSTHVPYTFGGG 255  
DB 182 PKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEADLGVYFCSQSTHVPYTFGGG 241  
QY 256 LEIK 259  
DB 242 LELK 245

RESULT 6  
US-10-112-788-9  
Sequence 9, Application US/10112788  
Publication No. US20030077676A1  
GENERAL INFORMATION:  
APPLICANT: DENARDO, SALLY  
APPLICANT: WINTHROP, MICHELLE  
APPLICANT: DENARDO, GERALD

;; TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING

;; FILE REFERENCE: 309T-000210US  
;; CURRENT APPLICATION NUMBER: US/10/112,788  
;; CURRENT FILING DATE: 2002-03-28  
;; PRIOR APPLICATION NUMBER: US 60/280,721  
;; PRIOR FILING DATE: 2001-04-30  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 9  
;; LENGTH: 281  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
;; US-10-112-788-9

Query Match 53.2%; Score 740.5; DB 9; Length 281;  
Best Local Similarity 58.1%; Pred. No. 4.1e-39;  
Matches 147; Conservative 32; Mismatches 61; Indels 13; Gaps 3;  
QY 14 AAHSFAAVALQSGAELVRPGASVTLSCASGYTFTDYEIHWVROTVPVHGLEWIGAIDP 73  
IDB 16 AAQPAMAQVQLQSGTEVWRPGASVKLSCKASGYFTSYDIDWVROTPEQGLEWIGWIFP 75  
QY 74 ETGCTAYNOKFKDAIVTVDKSSSTAYMELRLSLTSDSAVY-----YTRWFEDHGQGT 127  
DB 76 GEGSTEYNEKFKGRATLSVDKSSSTAYMELRLTSDSAVYFCARGDYRRYFDLWGQGT 135  
QY 128 LVTVAEGKSGSGSESKPG--DVVMTNPPLSLPVSLGDOASISCRSSQSLHSHNGITYLH 186  
IDB 136 TVTVSSRGGSGGGGGSDIELTQSPAIMSASPGERVMTCSASS-----TRYIY 189  
QY 187 WYLOKQSGPKLLIYKVNRFSGVDRFSGSGGTFTDLKISRVEAEDLGVYFCQSSTHV 246  
IDB 190 WYQKQKPGSPRLIYDTSNVAPGVPRFSGSGGTSLTINRMEADAATYYCQEWSGY 249  
QY 247 PYTFGGGTGLEIK 259  
DB 250 PYTFGGGTGLEIK 262

RESULT 7  
US-10-247-488-4  
;; Sequence 4, Application US/10247488  
;; Publication No. US2003002244A1  
;; GENERAL INFORMATION:  
;; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &  
;; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST MUTANT P53  
;; FILE REFERENCE: 1196336-RAMOT  
;; CURRENT APPLICATION NUMBER: US/10/247,488  
;; CURRENT FILING DATE: 2002-09-20  
;; PRIOR APPLICATION NUMBER: US/09/526,738  
;; PRIOR FILING DATE: 2000-03-16  
;; NUMBER OF SEQ ID NOS: 8  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 4  
;; LENGTH: 258  
;; TYPE: PRT  
;; ORGANISM: Humanus  
;; US-10-247-488-4

Query Match 52.5%; Score 730; DB 9; Length 258;  
Best Local Similarity 59.0%; Pred. No. 1.7e-38;  
Matches 144; Conservative 31; Mismatches 59; Indels 10; Gaps 3;  
QY 20 AAVALQSGAELVRPGASVTLSCASGYTFTDYEIHWVROTVPVHGLEWIGAIDPETGGTA 79  
DB 2 AQVKLQSGAELAKPGASVMSCKTSGYFTSTWMMVQRPQGLEWIGYINFTTYTK 61  
QY 80 YNQKFKDAIVTVDKSSSTAYMELRLSLTSDSAVYYT---RWFEDWGQGLTVTVAEGK 136  
DB 62 YNQKFKDAITLADKSSSTAYMQLSSLTNVDASVYCTTGYSYFDYWGQGTTVTVSSGG 121  
QY 137 SSGSGSESKPG--DVVMTNPPLSLPVSLGDOASISCRSSQSLHSHNGITYLH 195

DB 122 GSGGGSGGGSDIELTQSPAIMSASPGKEKVTITCSASS-----VNYMHWFQOKPGTS 175  
QY 196 PKLLIYKVNRFSGVDRFSGSGGTFTDLKISRVEAEDLGVYFCQSSTHVYTFGGGTGK 255  
DB 176 PKLWISSTSNLASGVPARFSGSGGTSLTISRNEADAATYYCQQRSSSYPTTFGGGTGK 235  
QY 256 LEIK 259  
DB 236 LQIK 239

RESULT 8  
US-09-880-748-1039  
;; Sequence 1039, Application US/09880748  
;; Publication No. US2003005937A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
;; FILE REFERENCE: PF523  
;; CURRENT APPLICATION NUMBER: US/09/880,748  
;; CURRENT FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-15  
;; PRIOR APPLICATION NUMBER: 60/240,816  
;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1039  
;; LENGTH: 260  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; US-09-880-748-1039

Query Match 52.5%; Score 730; DB 9; Length 260;  
Best Local Similarity 57.8%; Pred. No. 1.7e-38;  
Matches 149; Conservative 30; Mismatches 59; Indels 20; Gaps 4;  
QY 22 VOLQSGAELVRPGASVTLSCASGYTFTDYEIHWVROTVPVHGLEWIGAIDPETGGTAYN 81  
DB 2 VOLQSGPEVKKPGSSVKVSCRTSGTFRNYGLSWVRQAPGQGLEWGMGVIPISTIKYG 61  
QY 82 QKFKDAIVTVDKSSSTAYMELRLSLTSDSAVY-----YTRWF---EDWQO 125  
DB 62 QKFDRLTIVADDLTNTTYMELSLRPEDTAVVYCARAATTSQKHNYAYFYFGMDVMGR 121  
QY 126 GTLVTVAEGKSGSGSESKPG--DVVMTNPPLSLPVSLGDOASISCRSSQSLHSHNGI 182  
DB 122 GTITVSSGGSGGGGGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSG 181  
QY 183 TYLHWYLOKPGQSPKLLIYKVNRFSGVDRFSGSGGTFTDLKISRVEAEDLGVYFCQ 242  
DB 182 IYLDWYLOKPGQSPKLLIYKVNRFSGVDRFSGSGGTFTDLKISRVEAEDLGVYFCQ 241  
QY 243 STHVP-YTFGGGTGLEIK 259  
DB 242 ALHTPAITFGGTGLEIK 259

RESULT 9  
US-10-247-488-2  
;; Sequence 2, Application US/10247488  
;; Publication No. US2003002244A1  
;; GENERAL INFORMATION:  
;; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &  
;; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53  
;; FILE REFERENCE: 1196336-RAMOT  
;; CURRENT APPLICATION NUMBER: US/10/247,488



```

; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; TITLE OF INVENTION: Method for detecting lymphoid tissue involved in tumor progression
; FILE REFERENCE: Phy-03
; CURRENT APPLICATION NUMBER: US/09/940,391
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/244,369
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/077,970
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/073,882
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-940-191-1

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Query Match	51.0%	Score 709.5	DB 10	Length 244
Best Local Similarity	57.7%	Pred. No. 3e-37		
Matches 143	Conservative	30	Mismatches 66	Indels 9
			Gaps 3	

Qy	18	AFAAVLOQSGAELVRPGASVTLSCKASGYTFTDYBIEHVVROTPVHGLEWIGAIDPETGG	77
Db	1	AMGQVLOQSDAELVRPGASVKISCKASGYTFTDHAIHVMVKRPEQGLEWIGYFSPGND	60
Qy	78	TAYNOKFKDKAIVTDKSSSTAYMELRSLTSDSNAVYYTRM---	134
Db	61	IKYNEFKGKATLTADKSSSTAYMQLNSLTSDSNAVYFKRSYCNVDYMGQGTTLIVSSG	120
Qy	135	GKSGSGSGSEKPG-DVVMTPNPLVPSLGDQASISCRSSQSLHSHNGITYLHWYLQKSG	193
Db	121	GGSGGGGGGGCGGSDILLTQSPAILSVSPGERVSPFCRASQNI----	175
Qy	194	QSPKLLIKYVSNRFGSGGSGGTDTPLKISRVEAEDLGVFCSOSTHVPYTFGGG	253
Db	176	GSFRLLIKYASESVGIPSRFGSGGSGGTDTPLINSVESEDIAFYCQHTNSWPTTFGGG	235
Qy	254	TKLEIKEE	261
Db	236	TKLEIKLE	243

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RESULT 13
US-09-991-470-27
; Sequence 27, Application US/09991470
; Patent No. US20020173477A1
; GENERAL INFORMATION:
; APPLICANT: Ruey S. Liou
; TITLE OF INVENTION: ANTI-IGE GENE THERAPY
; FILE REFERENCE: 99-5
; CURRENT APPLICATION NUMBER: US/09/991,470
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/397,569
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 245
; TYPE: PRT
; ORGANISM: human/murine
US-09-991-470-27

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Query Match 50.9%; Score 708; DB 9; Length 245;  
Best Local Similarity 57.0%; Pred. No. 3.8e-37;  
Matches 142; Conservative 34; Mismatches 57; Indels 16; Gaps

Qy 22 VOLQQSGAELVRPGASVTLSCKASGYTFTDYEIHWVRQTPVHGLEWIGAIDPBTGGTAYN 81  
||| ||||| : ||||| : ||| : ||||| : ||| : |||  
Db 2 VOLVQSGAEVKKPGASVKVSKASGYTFSMYWLEWVRQAPGHGLEWVGISPGTFTTNYN 61

Qy	82	KQFKDAIVTVDKSSSTAYMELRSLTSEDASAVYYTR-----WFEDWGQGTLTVV	131
Db	62	EKFARATFTADTTNTAYMELSSLRSIEDTAVYVCARFSGHFSGNSVDYFDYWGGQLTVV	121
Qy	132	SAGKSSGSSESKEPG-DVVMTNPPLSPVLSCDQASISCRSQSLLHNGKITLYLHWYLQ	190
Db	122	SSGGSGSGGGGGGGSDILLTOSPTGLSLPGERATLSCRASQSI-----GTNIHWYQQ	176
Qy	191	KPGOSPALLIYKYVSNRFSGVPDRFSGSGGTDTFLKI SRVEAEALGVYFCSSOsthvpytf	250
Db	177	KPGCAPLLIKYASESIGIPSRFSGSGGTDTFLTISRLEPEDFAMVYCQSDSWPTTF	236
Qy	251	GGGTKUEIK	259
Db	237	GOGTKVEIK	245

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RESULT 14
US-09-880-748-1902
; Sequence 1902, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1902
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1902

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Query Match      50.8%; Score 706.5; DB 9; Length 245;
Best Local Similarity 55.6%; Pred.No. 4.7e-37;
Matches 138; Conservative 34; Mismatches 61; Indels 15; Gaps
4;

Qy    22  VQLQOSGAELVRPGASVTLSCAKSGYFTFDVEIHHWRQTTPVHGHLGIEWIGAIDPETGGTAYN 81
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    2  MOLVQSGAEVKKPGASVKVCKASKGYFTTSYMHWWVRQAPOGGLHMLGLVHPNDGSVNVA 61

Qy    82  QKFQDKAIVTVDKSSSTAYMELRSLTSEDSAVYYTYTR-----WPEF-WQGQGLTVTVS 132
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    62  QKFGRVTMTRTDSTSYVMELSSLRLSDDTAVVYCARDRGSGWPNWYFDLWGQGLTVTVS 121

Qy    133  AEKKSQSGSESXPG-DVVMTPTPLSPVLGDOASTISCRSSQLLSHNGITYLHHWYLQK 191
      :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db    122  SGGGSGGGSGGGGGDIQMTPSTUSASIGDRVITTCRASEGIGH-----WLAWYQQK 176

Qy    192  PGOSPILLIYKVNRPSGVDPDRFGSGSGGTDFTLKIIRVEAEDLGUVFCQSOTHPVYTFG 251

Db    177  PGRAPKLIIYKASSIASGPSPFSGSGSGGTDFTLTISSLRDDPATYLYCOOVSNYPITFG 236

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RESULT 15  
US-09-880-748-1778  
; Sequence 1778, Application US/09880748

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/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1778
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-880-748-1778

Query Match          50.8%; Score 706; DB 9; Length 248;
Best Local Similarity 55.4%; Pred. No. 5.le-37;
Matches 139; Conservative 34; Mismatches 60; Indels 18; Gaps 3;

QY 22 VLOQSGAELVRPGASVTLSCKASGYFTDYEHVVRQTPVHGLEWIGADPETGGTAYN 81
   |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 2 VLOQSGAEVRKPGASVKVCKASGYFTTSYGISWRQAPGHGLEWGWISAYNGNTNYA 61
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 82 QKFKDKAIVTVDKSSSTAYMELRSLTSEDGSAVYYVYTRWFED-----WGQGTLV 129
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 62 QKQGRVTMTDTSTAYMELRSLRSDDTAVYVCARSYYDILTGYPFGMDVWKGKTMV 121
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 130 TVSAEGKSGSGSGSEKPG-DVVMTPNPLSLPVSLGDAQSISCRSSQSLHNSGITYLHWY 188
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 122 TVSSGGGGGGGGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYH-----WLAWY 176
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 189 LQKPGQSPKLLIYKVSNRFSGVDPFRFGSGSGTDFTLKISRVEAEDLGVYFCQSQTHVPY 248
   |||||: :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 177 QKPKGAPKLLIYKASLASGAPRFGSGSGTDFTLTISLQPDPTATYYCQYSNYPL 236
   |||||: :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 249 TFGGGTKLEIK 259
   |||||: :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 237 TFGGGTKLEIK 247
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Search completed: May 16, 2003, 14:35:19  
Job time : 70 secs

GenCore version 5.1.4\_p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 14:22:00 ; Search time 29 Seconds  
(without alignments)  
272.923 Million cell updates/sec

Title: US-09-358-321C-32

Perfect score: 1391

Sequence: 1 MVSAILVYVLLAAAHSAFA.....FGGTTKLEKEKLISEEDL 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	928.5	66.8	367	1	US-08-257-341-5 Sequence 5, Appli
2	927.5	66.7	246	1	US-08-257-341-7 Sequence 7, Appli
3	927.5	66.7	252	1	US-08-133-804-4 Sequence 4, Appli
4	927.5	66.7	252	1	US-08-461-838-4 Sequence 4, Appli
5	927.5	66.7	252	2	US-08-461-838-4 Sequence 4, Appli
6	848.5	61.0	269	4	US-09-070-408-132 Sequence 132, App
7	830	59.7	288	4	US-09-423-439-38 Sequence 38, Appl
8	818.5	58.8	260	2	US-08-447-402-1 Sequence 1, Appli
9	806.5	58.0	247	4	US-09-227-693-34 Sequence 34, Appl
10	806.5	58.0	248	1	US-08-331-398A-34 Sequence 34, Appl
11	806.5	58.0	248	1	US-08-331-397B-34 Sequence 34, Appl
12	806.5	58.0	248	2	US-08-759-804A-34 Sequence 34, Appl
13	788.5	56.7	638	4	US-09-070-637-20 Sequence 20, Appl
14	788	56.6	535	4	US-08-983-035A-38 Sequence 38, Appl
15	779.5	56.0	673	4	US-09-423-439-32 Sequence 32, Appl
16	767	55.1	273	2	US-08-403-853-18 Sequence 18, Appl
17	762	54.8	365	3	US-08-875-811-53 Sequence 53, Appl
18	762	54.8	366	3	US-08-875-811-55 Sequence 55, Appl
19	761.5	54.7	281	4	US-09-025-769B-178 Sequence 178, App
20	761	54.7	271	2	US-08-894-922A-10 Sequence 10, Appl
21	755.5	54.3	263	2	US-08-752-844-66 Sequence 66, Appl
22	747	53.7	252	2	US-08-894-922A-14 Sequence 14, Appl
23	742	53.3	239	3	US-08-279-772A-8 Sequence 8, Appli
24	742	53.3	239	4	US-08-902-486-11 Sequence 11, Appl
25	741	53.3	553	2	US-08-263-911-7 Sequence 7, Appli
26	740.5	53.2	483	2	US-08-392-338A-19 Sequence 19, Appl
27	740.5	53.2	483	3	US-09-166-750-19 Sequence 19, Appl

28	740.5	53.2	483	3	US-09-166-093-19	Sequence 19, Appl
29	740.5	53.2	483	3	US-09-172-019-19	Sequence 19, Appl
30	740.5	53.2	483	3	US-09-166-094-19	Sequence 19, Appl
31	740	53.2	553	2	US-08-263-911-9	Sequence 9, Appli
32	739	53.1	289	3	US-09-184-658-63	Sequence 63, Appl
33	739	53.1	599	1	US-08-463-163-3	Sequence 3, Appli
34	728.5	52.4	244	2	US-08-553-497A-20	Sequence 20, Appl
35	726.5	52.2	246	2	US-08-553-497A-24	Sequence 24, Appl
36	720.5	51.8	281	4	US-09-423-439-44	Sequence 44, Appl
37	718	51.6	246	1	US-08-469-486-57	Sequence 57, Appl
38	718	51.6	246	2	US-08-469-658-57	Sequence 57, Appl
39	713.5	51.3	244	2	US-08-553-497A-22	Sequence 22, Appl
40	709.5	51.0	244	2	US-08-553-497A-26	Sequence 26, Appl
41	709.5	51.0	244	4	US-09-244-369B-1	Sequence 1, Appli
42	705	50.7	282	2	US-08-860-174A-10	Sequence 10, Appl
43	698.5	50.2	242	2	US-08-553-497A-28	Sequence 28, Appl
44	696.5	50.1	637	1	US-08-235-838-16	Sequence 16, Appl
45	696.5	50.1	637	2	US-08-465-473B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-257-341-5  
; Sequence 5, Application US/08257341  
; Patent No. 5525491  
; GENERAL INFORMATION:  
; APPLICANT: HUSTON, JAMES S  
; APPLICANT: OPPERMANN, HERMANN  
; APPLICANT: TIMASHEFF, SERGE N  
; TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CREATIVE BIOMOLECULES, INC./PATENT DEPT.  
; STREET: 35 SOUTH STREET  
; CITY: HOPKINTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 01748  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/257,341  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/842,149  
; FILING DATE:  
; APPLICATION NUMBER: US 07/662,226  
; FILING DATE: 27-FEB-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL ESQ, PAULA A  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: CRP-064CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/248-7000 (ATTY)  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 367 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-257-341-5

Query Match 66.8%; Score 928.5; DB 1; Length 367;

Best Local Similarity 74.7%; Pred. No. 1.1e-79;

Matches 189; Conservative 18; Mismatches 39; Indels 7; Gaps 3;

QY 13 AAHSAFAAVALQOOSGAELVRPGASVTLSCASGYTFTDYEIHWRQTPVHGLEWIGAID 72

115 AQAQKDEPELOQSGPELVKPGASVMSCKSGYIFDFYMNWVRQSHGKSLDYIGYIS 174  
173 PETGCTAYNQKFKDKAIVTVDKSSSTAYMELRSLTSDSAVYYY-----TRWFED-WGQG 126  
175 PYSQVTCYNQKFKGKATLTVDKSSSTAYMELRSLTSDSAVYYCAGSSGNKMWANDYWGCHG 234  
127 TLVTVAEGKSSGSGSKPGDVVMTNPLSLPVSLGDAQASISCRSSQSLHSHNGITYLH 186  
235 ASVTVSSSG-SSSSGSSSGSDVVMVTQTLPLSLPVSLGDAQASISCRSSQSLVHSHNGITYLN 293  
187 WYLOKPCQSKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGIVYFCQSSTHV 246  
294 WYLOKQCSKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGIVYFCQSSTHV 353  
247 PYTFGGGKLEIK 259  
354 PPTFGGKLEIK 366

## RESULT 2

US-08-257-341-7  
Sequence 7, Application US/08257341  
Patent No. 5525491  
GENERAL INFORMATION:  
APPLICANT: HUSTON, JAMES S  
APPLICANT: OPPERMAN, HERMANN  
APPLICANT: TIMASHEFF, SERGE N  
TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CREATIVE BIOMOLECULES, INC./PATENT DEPT.  
STREET: 35 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/257,341  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/842,149  
FILING DATE:  
APPLICATION NUMBER: US 07/662,226  
FILING DATE: 27-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, ESO, PAULA A  
REGISTRATION NUMBER: 32,503  
REFERENCE/DOCKET NUMBER: CRP-064CP  
TELEPHONE: 617/248-7000 (ATTY)  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 246 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-257-341-7

Query Match 66.7%; Score 927.5; DB 1; Length 246;  
Best Local Similarity 76.6%; Pred. No. 8e-80;  
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;  
22 VOLQOQGAELVRPGASVTLSCKASGYTFTDYEIHWVROTVPVHGLEWIGAIIDPETGTAYN 81  
3 VOLQOQGPVLKPGASVMSCKSGYIFDFYMNWVRQSHGKSLDYIGYISPYSGVTGN 62

QY 82 QKPKDKAIVTVDKSSSTAYMELRSLTSDSAVYYY-----TRWFED-WGQGLTVTVSAEG 135  
DB 63 QKPKGKATLTVDKSSSTAYMELRSLTSDSAVYYCAGSSGNKMWANDYWGCHGASVTVSSSG 122  
QY 136 KSSGSGSEKPGDVVMTNPLSLPVSLGDAQASISCRSSQSLHSHNGITYLHWHYLOKPGQS 195  
DB 123 -SSSSGSSSGSDVVMVTQTLPLSLPVSLGDAQASISCRSSQSLVHSHNGITYLNWYLOKAGOS 181  
QY 196 PKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGIVYFCQSSTHVPVTFGGGTK 255  
DB 182 PKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGIVYFCQSSTHVPVTFGGGTK 241  
QY 256 LEIK 259  
DB 242 LEIK 245

## RESULT 3

US-08-133-804-4  
Sequence 4, Application US/08133804  
Patent No. 5534254  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/133.804  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-133-804-4

Query Match 66.7%; Score 927.5; DB 1; Length 252;  
Best Local Similarity 76.6%; Pred. No. 8.3e-80;  
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;  
22 VOLQOQGAELVRPGASVTLSCKASGYTFTDYEIHWVROTVPVHGLEWIGAIIDPETGTAYN 81  
3 VOLQOQGPVLKPGASVMSCKSGYIFDFYMNWVRQSHGKSLDYIGYISPYSGVTGN 62  
QY 82 QKPKDKAIVTVDKSSSTAYMELRSLTSDSAVYYY-----TRWFED-WGQGLTVTVSAEG 135  
DB 63 QKPKGKATLTVDKSSSTAYMELRSLTSDSAVYYCAGSSGNKMWANDYWGCHGASVTVSSSG 122  
QY 136 KSSGSGSEKPGDVVMTNPLSLPVSLGDAQASISCRSSQSLHSHNGITYLHWHYLOKPGQS 195

Db 123 -SSSGSSSSGSDVVMVTQTPLSPVSLGDAQASISCRSSQSLVHNSGNTYLNWYLOKAGQS 181  
QY 196 PKLIYKVSNRFSVGPDRFSGSGGTDFTLKISRVEADLGIYFCSTHVPYTFGGGTK 255  
Db 182 PKLIYKVSNRFSVGPDRFSGSGGTDFTLKISRVEADLGIYFCSTHVPYTFGGGTK 241  
QY 256 LEIK 259  
Db 242 LEIK 245

RESULT 4  
US-08-461-838-4  
; Sequence 4, Application US/08461838  
; Patent No. 5753204  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For  
; TITLE OF INVENTION: Imaging  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461.838  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kelley, Robin D.  
; REGISTRATION NUMBER: 34,637  
; REFERENCE/DOCKET NUMBER: 2054/22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7477  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-461-838-4

Query Match 66.7%; Score 927.5; DB 1; Length 252;  
Best Local Similarity 76.6%; Pred. No. 8.3e-80;  
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;

QY 22 VLOQSGAELVRPGASVTLSCASGYTFTDYEIHVVRQTPVHGLEWICAIPTETGGTAYN 81  
Db 3 VLOQSGPELVKPCASVRMSCKSSGYITDFYMNVRQSHGKSLDIYIGISPYSGVTGYN 62  
QY 82 QKFKDQATVTDKSSSTAYMELRSLTSDSAVYY-----TRWFED-WGQTLTVTSAEG 135  
Db 63 QKFKGATLTVDKSSSTAYMELRSLTSDSAVYYCAGSSGNKNWANDYWGHSASVTVSSG 122  
QY 136 KSSGSGSESKPGDVMVTNPLSPVSLGDAQASISCRSSQSLVHNSGNTYLNWYLOKPGQS 195  
Db 123 -SSSGSSSSGSDVVMVTQTPLSPVSLGDAQASISCRSSQSLVHNSGNTYLNWYLOKAGQS 181  
QY 196 PKLIYKVSNRFSVGPDRFSGSGGTDFTLKISRVEADLGIYFCSTHVPYTFGGGTK 255

Db 182 PKLIYKVSNRFSVGPDRFSGSGGTDFTLKISRVEADLGIYFCSTHVPYTFGGGTK 241  
QY 256 LEIK 259  
Db 242 LEIK 245

RESULT 5  
US-08-461-386-4  
; Sequence 4, Application US/08461386  
; Patent No. 5837846  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For  
; TITLE OF INVENTION: Imaging  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461.386  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kelley, Robin D.  
; REGISTRATION NUMBER: 34,637  
; REFERENCE/DOCKET NUMBER: 2054/22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7477  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-461-386-4

Query Match 66.7%; Score 927.5; DB 2; Length 252;  
Best Local Similarity 76.6%; Pred. No. 8.3e-80;  
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;

QY 22 VLOQSGAELVRPGASVTLSCASGYTFTDYEIHVVRQTPVHGLEWICAIPTETGGTAYN 81  
Db 3 VLOQSGPELVKPCASVRMSCKSSGYITDFYMNVRQSHGKSLDIYIGISPYSGVTGYN 62  
QY 82 QKFKDQATVTDKSSSTAYMELRSLTSDSAVYY-----TRWFED-WGQTLTVTSAEG 135  
Db 63 QKFKGATLTVDKSSSTAYMELRSLTSDSAVYYCAGSSGNKNWANDYWGHSASVTVSSG 122  
QY 136 KSSGSGSESKPGDVMVTNPLSPVSLGDAQASISCRSSQSLVHNSGNTYLNWYLOKPGQS 195  
Db 123 -SSSGSSSSGSDVVMVTQTPLSPVSLGDAQASISCRSSQSLVHNSGNTYLNWYLOKAGQS 181  
QY 196 PKLIYKVSNRFSVGPDRFSGSGGTDFTLKISRVEADLGIYFCSTHVPYTFGGGTK 255  
Db 182 PKLIYKVSNRFSVGPDRFSGSGGTDFTLKISRVEADLGIYFCSTHVPYTFGGGTK 241  
QY 256 LEIK 259  
Db 242 LEIK 245



```

US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
;           BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NO. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
;
US-09-423-439-38

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Query Match      59.7%; Score 830; DB 4; Length 288;
Best Local Similarity 64.2%; Pred. No. 1.6e-70;
Matches 174; Conservative 30; Mismatches 55; Indels 12; Gaps

Qy      10  L L A A A H S A P A A V Q L O Q S G A E L V R P C A S Y T L S C K A S G Y T F T D Y E I H W R Q T P V H G L E W I G 69
      Db      12  L L L L A A Q P A M A Q V O L Q P C A E L V K P C A S V Q L S C K A S G Y T F T G Y I H W R Q P Q O G L E W I G 71

Qy      70  A I D P E T G C T A Y N O K F D K A I L V T V D K S S T A Y M E L R S L T S E D S A V Y Y T R - - - - W F E D - - - 122
      Db      72  E V N P S T G R S D Y N E K F K N K A T L V T V D K S S T A Y M Q L S S L T S E D S A V Y Y C A R E A Y G Y D D A M D 131

Qy      123 - W Q Q G L T V T V A S E K S G S G S E S K P G - D V V M T P N P L S L P V S L G D Q A S I C R S S Q S L H S - 179
      Db      132 Y M Q G T T V T V S S G G G S G G G G G G S D I E L S Q S P S L A V S A G E K V T M C K S Q S L N S R 191

Qy      180 N G I T Y L H W Y L O K P Q S P K L I Y K V S N R F S G V P D R F S G S G G T D F T L K I S R V A E D L G V Y F 239
      Db      192 T R A N Y L A W Y O O R P Q S P K L I Y W A S T R T S G V P D R F T G S G S G T D F T L T I S V Q A E D L A I Y F 251

Qy      240 C S Q S T H V P T F G G G T K L E I K - E K L I S E D L 269
      Db      252 C K O S - Y L R T F G G G T K L E I K R E O K L I S E D L 281

```

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RESULT 8
US-08-447-402-1
; Sequence 1, Application US/08447402
; Patent No. 5866344
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; APPLICANT: Georgiou, George
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: IMMUNOASSAY AND ANTIBODY SELECTION

```

		Query Match	61.0%; Score 848.5; DB 4;	Length 269;
		Best Local Similarity	69.7%; Pred. No. 2.6e-72;	
		Matches 170; Conservative 23;	Mismatches 44;	Indels 7; Gaps
2Y	22	VQLQSGAELVRPGASVTLSCKASGYTFTDYEIHWVROTPTVHGLEWIGAI	IDPETGGTAYN	81
bB	3	VLOQSGPELVKPGASVRMSCKSSGYIFTDFYMWVRQSHGKSLDYIVISPY	SGVTGVN	62
2Y	82	OKFKDKAIVTVDKSSSTAYMELRSLTSEDSAVYY-----TRWFED-W	QGCTLTVTVSAG	135
bB	63	QKFPGKATLTVDKSSSTAYMELRSLTSEDSAVYICAGSGNKWAMDYHG	GASVTSSOG	122
2Y	136	KSSGGSSESKEPG-DVVMTNPPLSPVSLGDQASISCRSOSLLHSNGIT	YLHWYLOKPCQ	194
bB	123	GGSGGGGGGGGSDIVLTOTPPSLPVLGDQATISCRSOSLVHNSNGTY	LAWYLOKAGO	182
2Y	195	SPKLLIYKVSNRFGVPDRPFSSGSGGTDTFLKISRVEADLGVIYFC	SQTHVPYTFGGT	254
bB	183	SPKLLIYKVSNRFGVGPAPFSGSGGSDFTLIIDRVVEDAAIYCSQT	HVPPTFGSGT	242
2Y	255	KLEI	258	
bB	243	KLEI	246	
		RESULT	7	

## TITLE OF INVENTION: METHODS USING CELL SURFACE EXPRESSED

LIBRARIES

TITLE OF INVENTION: METHODS USING CELL SURFACE EXPRESSED

LIBRARIES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold, White &amp; Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/447,402

FILING DATE: 23-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/258,543

FILING DATE: 10-JUN-1994

CLASSIFICATION: 424

APPLICATION NUMBER: 07/794,731

FILING DATE: 15-NOV-1991

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: UT58\584\KIT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 260 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-447-402-1

Query Match 58.8%; Score 818.5; DB 2; Length 260;

Best Local Similarity 66.9%; Pred. No. 1.7e-69;

Matches 164; Conservative 26; Mismatches 48; Indels 7; Gaps 3;

QY 22 VOLQOQSGAELVRPGASVTLSCKASGYTFTDYEIHWVROTTPVHGLEWIGAIIDPETGGTAYN 81

DB 2 VOLQOQSGPELVKPGASVVMCKSSGYIFDYMNVKQSHGKSLDYGISPSYSGVTGYN 61

QY 82 QKPKDKAIVTVDKSSSTAYMELRSLTSEDSAVYYY-----TRWPEF-WGQGLTVTVSAEG 135

DB 62 QKPKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSGNKAWDYWGHCASVTVSSGG 121

QY 136 KSSGSGSESKPG-DVWMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQ 194

DB 122 GSGSGSGSGGGSDIVLTQSPASLAVSLGQRATISCRSSQSLVHNSGNTYLNWYQKPGQ 181

QY 195 SPKLLIYKVSNRFGVDPDRFSGSGSGDFTLTKISRVAEDLGIVYFCQSOTHPVTFGGGT 254

DB 182 PKKLLIYKVSNRFGVDPDRFSGSGSGDFTLTKISRVAEDLGIVYFCQSOTHPVTFGGGT 241

QY 255 KLEIK 259

DB 242 KLEIK 246

RESULT 9

US-09-227-693-34

Sequence 34, Application US/09227693

Patent No. 6287562

GENERAL INFORMATION:

APPLICANT: PASTAN, Ira

APPLICANT: BENHAR, Itai

APPLICANT: PADLAN, Eduardo A.

APPLICANT: JUNG, Sun-Hee

APPLICANT: LEE, Byungkook

TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY

TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: Steuart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/227,693

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/331,396

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 15280-126-1-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-227-693-34

Query Match 58.0%; Score 806.5; DB 4; Length 247;

Best Local Similarity 63.7%; Pred. No. 2.1e-68;

Matches 156; Conservative 29; Mismatches 53; Indels 7; Gaps 2;

QY 22 VOLQOQSGAELVRPGASVTLSCKASGYTFTDYEIHWVROTTPVHGLEWIGAIIDPETGGTAYN 81

DB 3 VLVESGGGLVQPGGSLKLSKATSGFTFSDYMYWVYRQTPEKRLWVAYISNDSSAAYS 62

QY 82 QKPKDKAIVTVDKSSSTAYMELRSLTSEDSAVYYYR-----WFDWGQGLTVTVSAEG 135

DB 63 DTYKGRFTISRDNARNTLYLQMGRLKSEDTAIYSCARGLAWGAWFAYWGQGLTVTVSSGG 122

QY 136 KSSGSGSESKPG-DVWMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQ 194

DB 123 GSGSGSGSGGGSDIVLTQSPASLAVSLGQASISCRSSQIIVHNSGNTLYLWYLOKPGQ 182

QY 195 SPKLLIYKVSNRFGVDPDRFSGSGSGDFTLTKISRVAEDLGIVYFCQSOTHPVTFGGGT 254

DB 183 SPKLLIYKVSNRFGVDPDRFSGSGSGDFTLTKISRVAEDLGIVYFCQSOTHPVTFGGGT 242

QY 255 KLEIK 259

DB 243 KLEIK 247

RESULT 10

US-08-331-398A-34

Sequence 34, Application US/08331398A  
Patent No. 5608039  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark  
APPLICANT: FitzGerald, David  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pal, Lee  
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
TITLE OF INVENTION: and Their Uses (as amended)  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,398A  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-1261100S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-331-398A-34

Query Match 58.0%; Score 806.5; DB 1; Length 248;  
Best Local Similarity 63.7%; Pred. No. 2.1e-68;  
Matches 156; Conservative 29; Mismatches 53; Indels 7; Gaps 2;  
2y 22 VQLQSGAELVRPGASVTLSCASGYTFTDYEIHWVROTYPVHGLEWICAIIDPETGCTAYN 81  
Db 3 VLVESGGGLVQPGSLKSLCATSGTFFSDYIMYWRQIPKRLWVAYISNDSSAAYS 62  
2y 82 QKFKOKAIVTVDKSSSTAYMELRLSTSDSAVYYTR-----WFDWMGQGLTVTVSAEG 135  
Db 63 DTWKGRFTISRDNARNTLYLQMSRLKSEDTAIYSCARGLAWGAWFAYWGQGLTVTVSSGG 122  
2y 136 KSSGSGSEKPG-DVWMTNPNLSLPVSLGDAQASISCRSSQSLHNSNGITYLHWYLOKPGQ 194  
Db 123 GSGSGGGGGGGSDVLMQTSPLSLPVSLGDAQASISCRSSQIIVHNSNGNTYLEWYLOKPGQ 182  
2y 195 SPKLLIYKVNRFSGVDPDRFSGSGSGTDTLTKISRVEADLGVYFCSTHVPYTFGGGT 254  
Db 183 SPKLLIYKVNRFSGVDPDRFSGSGSGTDTLTKISRVEADLGVYFCSTHVPYTFGGGT 242  
2y 255 KLEIK 259  
Db 243 KLEIK 247

RESULT 11  
US-08-331-397B-34  
Sequence 34, Application US/08331397B  
Patent No. 5981726  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Benhar, Itai  
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,397B  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-1261200S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-331-397B-34

Query Match 58.0%; Score 806.5; DB 2; Length 248;  
Best Local Similarity 63.7%; Pred. No. 2.1e-68;  
Matches 156; Conservative 29; Mismatches 53; Indels 7; Gaps 2;  
Qy 22 VQLQSGAELVRPGASVTLSCASGYTFTDYEIHWVROTYPVHGLEWICAIIDPETGCTAYN 81  
Db 3 VLVESGGGLVQPGSLKSLCATSGTFFSDYIMYWRQIPKRLWVAYISNDSSAAYS 62  
Qy 82 QKFKOKAIVTVDKSSSTAYMELRLSTSDSAVYYTR-----WFDWMGQGLTVTVSAEG 135  
Db 63 DTWKGRFTISRDNARNTLYLQMSRLKSEDTAIYSCARGLAWGAWFAYWGQGLTVTVSSGG 122  
Qy 136 KSSGSGSEKPG-DVWMTNPNLSLPVSLGDAQASISCRSSQSLHNSNGITYLHWYLOKPGQ 194  
Db 123 GSGSGGGGGGGSDVLMQTSPLSLPVSLGDAQASISCRSSQIIVHNSNGNTYLEWYLOKPGQ 182  
Qy 195 SPKLLIYKVNRFSGVDPDRFSGSGSGTDTLTKISRVEADLGVYFCSTHVPYTFGGGT 254  
Db 183 SPKLLIYKVNRFSGVDPDRFSGSGSGTDTLTKISRVEADLGVYFCSTHVPYTFGGGT 242  
Qy 255 KLEIK 259  
Db 243 KLEIK 247

RESULT 12  
US-08-759-804A-34  
; Sequence 34, Application US/08759804A  
; Patent No. 5990296  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark  
; APPLICANT: Fitzgerald, David J.  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Pai, Lee  
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,  
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US 08/331,398  
; FILING DATE: 28-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-126140US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-759-804A-34

Query Match 58.0%; Score 806.5; DB 2; Length 248;  
Best Local Similarity 63.7%; Pred. No. 2.1e-66;  
Matches 156; Conservative 29; Mismatches 53; Indels 7; Gaps 2;  
QY 22 VOLQOQGAELVRPGASVTLSCKASGYTFDYEIHWVROTYPVHGLEWIGADIPETGGTAYN 81  
DB 3 KLVESGGGLVQPGSLKSLCATSGTFSDYMYWVROTPEKRLIEWAYINSDSSAAYS 62  
QY 82 QKFKDKAIVTVDKSSSTAYMELRLSTSEDSAVYYTR-----WFDWGQGTTLTVSAEG 135  
DB 63 DTVKGRFTISRDNARNTLYLQMSRLKSEDTAIYSCARGLANWAFYWGQGTTLTVSSGG 122  
QY 136 KSSGSGSEKPG-DVWMTNPLSLPVSGLDQASISCRSSQSLHNSGITYLHWYLRPGQ 194  
DB 123 GSGGGGGGGGGSDVLMTQSPSLPVSGLDQASISCRSSQIIVHNSGNTYLEWYLRPGQ 182  
QY 195 SPKLLIYKVSNNRFGVDPDRFSGSGGTDFTLKISRVEAEDLGVVFCQSOSTHVPYTFGGGT 254  
DB 183 SPKLLIYKVSNNRFGVDPDRFSGSGGTDFTLKISRVEAEDLGVVYFCQSHVPTFGSGT 242

QY 255 KLEIK 259  
DB 243 KLEIK 247  
RESULT 13  
US-09-070-637-20  
; Sequence 20, Application US/09070637A  
; Patent No. 6132722  
; GENERAL INFORMATION:  
; APPLICANT: SIEMERS, NATHAN O.  
; APPLICANT: YARNOLD, SUSAN  
; APPLICANT: SENTER, PETER D.  
; TITLE OF INVENTION: RECOMBINANT ANTIBODY-ENZYME FUSION PROTEINS  
; FILE REFERENCE: 9197F-83-1  
; CURRENT APPLICATION NUMBER: US/09/070,637A  
; CURRENT FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: 60/045,888  
; EARLIER FILING DATE: 1997-05-07  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 638  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
; OTHER INFORMATION: sequence for L49-sfv-bl including Pe1B leader  
US-09-070-637-20

Query Match 56.7%; Score 788.5; DB 4; Length 638;  
Best Local Similarity 60.4%; Pred. No. 3.9e-66;  
Matches 165; Conservative 31; Mismatches 60; Indels 17; Gaps 5;  
QY 10 LLAASAAFAAVLOQSGAELVRPGASVTLSCKASGYTFDYEIHWVROTYPVHGLEWIG 69  
DB 12 LLLAOPAAEVOQESGSLVKPSTLSTCSVTGDSITSGVWNRKFPNGKLEYMG 71  
QY 70 AIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRLSTSEDSAVY-----YYTRWF 120  
DB 72 YIS-DSGITYNPSLSKRSITRDTSKNQVYLQNFVTAEDTATYNCARRTLATYYA--M 128  
QY 121 EDWGQGTTLTVSAEGKSS-----CGSESKEPGDVVMTNPLSLPVSGLDQASISCRSSQSL 176  
DB 129 DYWGQGTSTVTVSSG 188  
QY 177 LHSNGITYLHWYLRPGQSPKLLIYKVSNNRFGVDPDRFSGSGGTDFTLKISRVEAEDLG 236  
DB 189 VHSNGNTYLHWYLRPGQSPKLLIYKVSNNRFGVDPDRFSGSGGTDFTLKISRVEAEDLG 248  
QY 237 VYFCQSOSTHVPYTFGGGTTLKLEKEKLISEEDL 269  
DB 249 VYFCQSOSTHVPYTFGGGTTLKLEIKRTP-VSEKQL 280

RESULT 14  
US-08-983-035A-38  
; Sequence 38, Application US/08983035A  
; Patent No. 6326464  
; GENERAL INFORMATION:  
; APPLICANT: CONSEILLER, EMMANUEL  
; BRACCO, LAURENT  
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
; USES THEREOF  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
; DUNNER, LLP  
; STREET: 1300 I Street, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,035A  
FILING DATE: 20-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/01111  
FILING DATE: 17-JUL-1996  
APPLICATION NUMBER: FR 95/08729  
FILING DATE: 19-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Strauss, William L.  
REGISTRATION NUMBER: 47,114  
REFERENCE/DOCKET NUMBER: 03804.0142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-08-983-035A-38

Query Match 56.6%; Score 788; DB 4; Length 535;  
Best Local Similarity 65.2%; Pred. No. 3.4e-66;  
Matches 159; Conservative 24; Mismatches 57; Indels 4; Gaps 2;

QY 20 AAVQLQSGAELVPCASVTLSCASGYTFTDYEIHWVROTPVHGLEWICADPETGGTA 79  
DB 2 AQVQLSGAELVPCASVTLSCASGYTFTDYEIHWVROTPVHGLEWICADPETGGTA 61

QY 80 YNOKFKDKAIVTVDKSSSTAYMELRLTSDSAVY---YTRWFEDWGQOTLVTVSAEGK 136  
DB 62 YAPKFGKATMTADTSNTAYLQLSLASEDTAVYYCNFYGDALDWGQOTLVTVSSGGG 121

QY 137 SSGSGSEKPG-DVWTPNPLSLPVLGDOASISCRSSOSLLHSGITLHNYLQKPGOS 195  
DB 122 GSGGGSGGGGSDVLTQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLNMLLQRPQOS 181

QY 196 PKLLIYKVNRFSGVDFRFGSGGSDFTLKISRVEADLGVYFCQSOSTHVPYTFGGTK 255  
DB 182 PKRLIYLVSKLSDGVDFRFGSGGSDFTLKISRVEADLGVYFCQSOSTHVPYTFGGTK 241

QY 256 LEIK 259  
DB 242 LEUK 245

RESULT 15  
US-09-423-439-32  
Sequence 32, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-No. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-423-439-32

Query Match 56.0%; Score 779.5; DB 4; Length 673;  
Best Local Similarity 61.1%; Pred. No. 2.9e-65;  
Matches 160; Conservative 32; Mismatches 59; Indels 11; Gaps 5;

QY 8 YVLLAAAHSAFAAVALQOOSGAELVPCASVTLSCASGYTFTDYEIHWVROTPVHGLEW 67  
DB 7 WIFLVTLINGIQCVQLQOPGAELVPCASVTLSCASGYTFTGWIHWKORPQGGLEW 66

QY 68 IGAIIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRLTSDSAVY---WFED- 122  
DB 67 ICEVNPSTGRSDYNEKFKNKATLTVDKSTTAYMQLSSLTSDSAVYCARERAYCYDDA 126

QY 123 ---WCOGTLVTVSAEKGSGSGSEKPG-DVWMTNPLSLPVLGDOASISCRSSOSLLH 178  
DB 127 MDYWGQGTITVTVSSGGGSGGGGSDIELSOSPSSLAVSAGEKVTMSCKSSQSLLN 186

QY 179 S-NGITYLHWYLVKQKPGSPKLLIYKVNRFSGVDFRFGSGGSDFTLKISRVEADLGV 237  
DB 187 SSTRKNYLANWQORFGQSPKLLIYWASTRTSGVDFRFGSGGSDFTLTISVQAEADLAI 246

QY 238 YFCQSOSTHVPYTFGGTKLEIK 259  
DB 247 YYCKQS-YTLRTFGGTTKLEIK 267

Search completed: May 16, 2003, 14:26:53  
Job time : 32 secs